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## HEREGULIN VARIANTS

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BACKGROUND OF THE INVENTIONField of the Invention

The present invention relates to heregulin variants, nucleic acid molecules encoding such variants, and related vectors, host cells, pharmaceutical compositions, and methods.

In particular, the invention relates to amino acid substitution variants of human heregulin- $\beta$ 1 having an enhanced affinity for the ErbB-3 and ErbB-4 receptors.

5    Description of the Related Art

Transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases are enzymes that catalyze this process. Receptor protein tyrosine kinases are believed to direct cellular growth via ligand-stimulated tyrosine phosphorylation of intracellular proteins. Growth factor receptor protein tyrosine kinases of the class I subfamily include the 170 kilodalton (kDa) epidermal growth factor receptor (EGFR) encoded by the erbB1 gene. erbB1 has been causally implicated in human malignancy. In particular, increased expression of this gene has been observed in more aggressive carcinomas of the breast, bladder, lung, and stomach.

The second member of the class I subfamily, p185<sup>neu</sup> (also called the ErbB-2 receptor or p185<sup>HER2</sup>), was originally identified as the product of the transforming gene from neuroblastomas of chemically treated rats. The neu (erbB2 or HER2) gene encodes a 185 kDa receptor protein tyrosine kinase.

Amplification and/or overexpression of the human erbB2 gene correlates with a poor prognosis in breast and ovarian cancers. Slamon et al., *Science* 235:177-82 (1987); Slamon et al., *Science* 244:707-12 (1989). Overexpression of erbB2 has been correlated with other carcinomas including carcinomas of the stomach, endometrium, salivary gland, lung, kidney, colon and bladder. Accordingly, in U.S. Patent No. 4,968,603, Slamon et al. describe and claim various diagnostic assays for determining erbB2 gene amplification or expression in tumor cells. Slamon et al. discovered

that the presence of multiple copies of the erbB2 oncogene in tumor cells indicates that the disease is more likely to spread beyond the primary tumor site, and that the disease may therefore require more aggressive treatment than might otherwise be indicated by other diagnostic factors. Slamon et al. conclude that the erbB2 gene amplification test, together with the determination of lymph node status, provides greatly improved prognostic utility.

A further related gene, called erbB3 (or HER3), which encodes the ErbB-3 receptor ( $p180^{HER3}$ ) has also been described. See U.S. Patent No. 5,183,884; Kraus et al., *PNAS USA* 86:9193-97 (1989); EP Patent Application No. 444,961A1; Kraus et al., *PNAS USA* 90:2900-04 (1993). Kraus et al. (1989) discovered that markedly elevated levels of erbB3 mRNA were present in certain human mammary tumor cell lines indicating that erbB3, like erbB1 and erbB2, may play a role in human malignancies. Also, Kraus et al. (1993) showed that EGF-dependent activation of the ErbB-3 catalytic domain of a chimeric EGFR/ErbB-3 receptor resulted in a proliferative response in transfected NIH-3T3 cells. Furthermore, these researchers demonstrated that some human mammary tumor cell lines display a significant elevation of steady-state ErbB-3 receptor tyrosine phosphorylation, further implicating this receptor in human malignancies. The role of erbB3 in cancer has been explored by others, and this gene has been found to be overexpressed in breast (Lemoine et al., *Br. J. Cancer* 66:1116-21 [1992]), gastrointestinal (Poller et al., *J. Pathol.* 168:275-80 [1992]; Rajkumar et al., *J. Pathol.* 170:271-78 [1993]; Sanidas et al., *Int. J. Cancer* 54:935-40 [1993]), and pancreatic cancers (Lemoine et al., *J. Pathol.* 168:269-73 [1992], and Friess et al., *Clinical Cancer Research* 1:1413-20 [1995]).

The class I subfamily of growth factor receptor protein tyrosine kinases has been further extended to include the ErbB-4 (HER4) receptor, which is the product of the erbB4 (HER4) gene. See EP Patent Application No. 599,274; Plowman et al., *PNAS USA* 90:1746-50 (1993); and Plowman et al., *Nature* 366:473-75 (1993). Plowman et al. found that increased erbB4 expression closely correlated with certain carcinomas of epithelial origin, including breast adenocarcinomas.

Diagnostic methods for detection of human neoplastic conditions (especially breast cancers) that evaluate erbB4 expression are described in EP Patent Application No. 599,274.

The quest for the activator of the erbB2 oncogene has lead to the discovery of a family of heregulin polypeptides. In humans, the heregulin polypeptides characterized thus far are derived from alternate splicing of a single gene which was mapped to the short arm of chromosome 8 by Lee and Wood, *Genomics* 16:790-91 (1993).

Holmes et al. isolated and cloned a family of polypeptide activators for the ErbB-2 receptor which they called heregulin- $\alpha$  (HRG- $\alpha$ ), heregulin- $\beta$ 1 (HRG- $\beta$ 1), heregulin- $\beta$ 2 (HRG- $\beta$ 2), and heregulin- $\beta$ 3 (HRG- $\beta$ 3). See Holmes et al., *Science* 256:1205-10 (1992); WO 92/20798; and U.S. Patent No. 5,367,060. These researchers demonstrated the ability of the purified heregulin polypeptides to activate tyrosine phosphorylation of the ErbB-2 receptor in MCF7 breast tumor cells. Furthermore, the mitogenic activity of the heregulin polypeptides on SK-BR-3 cells (which express high levels of the ErbB-2 receptor) was also demonstrated.

Heregulins are large multi-domain proteins that are typically expressed as "pro-heregulins." Pro-heregulins have been shown to undergo proteolytic processing to a mature soluble form (usually of about

44-45 kDa). Processing has been shown to occur intracellularly or at the cell surface. Domains in the soluble form include (in order from the N- to the C-terminus) an immunoglobulin homology (Ig-like) domain, a spacer region rich in glycosylation sites, and a domain similar to a domain found in EGF that is sufficient for ErbB receptor binding and activation. See Barbacci, et al., *J. Biol. Chem.* 270:9585-89 (1995).

10 The heregulin EGF-like domains are characterized by substantial structural similarities to (Jacobsen et al., *Biochemistry* 35:3402-17 [1996]), and limited sequence homology with, EGF residues 1-48 (Holmes, et al., *supra*). Functional similarities between the  
15 heregulin EGF-like domains and EGF have been established by data showing that blocks of EGF sequence substituted into heregulin- $\beta$ 1 do not impair binding to cells co-expressing ErbB-3 and ErbB-2. Barbacci et al., *supra*.

20 While heregulins are substantially identical in the first 213 amino acid residues, they are classified into two major types,  $\alpha$  and  $\beta$ , based on two EGF-like domains that differ in their C-terminal portions. For example, the heregulin- $\alpha$  EGF-like domain differs from  
25 that of the  $\beta$ 1-isoform by nine substitutions near the C-terminus. The  $\beta$ -isoform has been reported to bind ErbB receptors with approximately eight to 10-fold higher affinity than the  $\alpha$ -isoform. Wen et al., *Mol. Cell. Biol.* 14:1909-19 (1994).

30 The solution structure of the heregulin- $\alpha$  EGF domain has recently been determined at high resolution by NMR. Jacobsen et al., *supra*; Nagata et al., *EMBO J.* 13, 3517-3523 (1994). The salient features of this domain include (1) an N-terminal subdomain containing a  
35 central three-stranded  $\beta$ -sheet with an intermittent helix and (2) a smaller C-terminal subdomain that contains a short stretch of  $\beta$ -sheet. The EGF domain is

stabilized by three disulfide bonds, two in the N-terminal subdomain and one in the C-terminal subdomain. The pairing of the six corresponding cysteine residues is conserved in EGF-like domains from 5 all heregulins and from EGF.

The 44 kDa *neu* differentiation factor (NDF), which is the rat equivalent of human HRG, was first described by Peles et al., *Cell*, 69:205-16 (1992), and Wen et al., *Cell*, 69:559-72 (1992). Like the human heregulin polypeptides, NDF has an Ig-like domain followed by an EGF-like domain and lacks a N-terminal signal peptide. Subsequently, Wen et al. carried out "exhaustive cloning" to extend the family of NDFs. Wen et al., *Mol. Cell. Biol.*, 14:1909-19 (1994). This work 10 revealed six distinct fibroblastic pro-NDFs. Adopting the nomenclature of Holmes et al., the NDFs were 15 classified as either  $\alpha$  or  $\beta$  polypeptides based on the sequences of the EGF-like domains. Isoforms 1 to 4 are characterized on the basis of a variable region between 20 the EGF-like domain and transmembrane domain. Also, isoforms a, b and c are defined based on variable-length cytoplasmic domains. These researchers conclude 25 that different NDF isoforms are generated by alternative splicing and perform distinct tissue-specific functions. See also EP 505 148; WO 93/22424; and WO 94/28133 (discussing NDF).

Falls et al., *Cell* 72:801-815 (1993) describe another member of the heregulin family which they call "acetylcholine receptor inducing activity (ARIA) 30 polypeptide." The chicken-derived ARIA polypeptide stimulates synthesis of muscle acetylcholine receptors. See WO-94/08007. ARIA is a  $\beta$ -type heregulin and lacks the entire spacer region between the Ig-like domain and EGF-like domain of HRG- $\alpha$  and HRG $\beta 1-\beta 3$ .

35 Marchionni et al., *Nature* 362:312-318 (1993) identified several bovine-derived proteins that they call "glial growth factors (GGFs)." These GGFs share

the Ig-like domain and EGF-like domain with the other heregulin proteins described above, but also have an amino-terminal kringle domain. GGFs generally do not have the complete spacer region between the Ig-like domain and EGF-like domain. Only one of the GGFs, GGFII, has an N-terminal signal peptide. See also WO 92/18627; WO 94/00140; WO 94/04560; WO 94/26298; WO 95/32724 (describing GGFs and uses thereof).

Ho et al. describe another member of the heregulin family called "sensory and motor neuron-derived factor (SMDF)." Ho et al., *J. Biol. Chem.* 270:14523-32 (1995). This protein has an EGF-like domain characteristic of all other heregulin polypeptides but a distinct N-terminal domain. In addition, SMDF lacks both the Ig-like domain and the spacer region found in other heregulin polypeptides. Another feature of SMDF is the presence of two stretches of hydrophobic amino acids near the N-terminus.

While the heregulin polypeptides were first identified based on their ability to activate the ErbB-2 receptor (see Holmes et al., *supra*), it has been discovered that certain ovarian cells expressing neu (erbB2) and neu-transfected fibroblasts did not bind or crosslink to NDF, nor did they undergo tyrosine phosphorylation in response to NDF. Peles et al., *EMBO J.* 12:961-71 (1993). This finding indicated that another cellular component was necessary for conferring full heregulin responsiveness.

Carraway et al. subsequently demonstrated that <sup>125</sup>I-rHRG- $\beta$ 1 177-244 bound to NIH-3T3 fibroblasts stably transfected with bovine erbB3 but not to non-transfected parental cells. These researchers also expressed bovine ErbB-3 receptor in insect cells and showed that HRG- $\beta$ 1 177-244 bound to a preparation of ErbB-3 receptor solubilized from these cells. They concluded that ErbB-3 is a receptor for heregulin and mediates phosphorylation of intrinsic tyrosine residues

as well as phosphorylation of ErbB-2 receptor in cells that express both receptors. Carraway et al., *J. Biol. Chem.* 269:14303-06 (1994). Sliwkowski et al. found that cells transfected with erbB3 alone show low 5 affinities for heregulin, whereas cells transfected with both erbB2 and erbB3 show higher affinities. Sliwkowski et al., *J. Biol. Chem.* 269:14661-65 (1994).

Plowman and his colleagues have similarly studied ErbB-4/ErbB-2 receptor activation. They expressed the 10 ErbB2 receptor alone, the ErbB4 receptor alone, or the two receptors together in human T lymphocytes and demonstrated that heregulin is capable of stimulating tyrosine phosphorylation of ErbB-4, but could only stimulate ErbB-2 phosphorylation in cells expressing 15 both receptors. Plowman et al., *Nature* 336:473-75 (1993).

These observations are consistent with the "receptor cross-talking" concept described previously by Kokai et al., *Cell* 58:287-92 (1989), Stern et al., 20 *EMBO J.* 7:995-1001 (1988), and King et al., 4:13-18 (1989). These researchers found that binding of EGF to the EGFR resulted in activation of the EGFR kinase domain and cross-phosphorylation of the ErbB-2 receptor. This is believed to be a result of ligand- 25 induced receptor heterodimerization and the concomitant cross-phosphorylation of the receptors within the heterodimer. Wada et al., *Cell* 61:1339-47 (1990).

Thus, the ErbB receptors are believed to be activated by ligand-induced receptor dimerization. 30 Specifically, heregulins can bind separately to ErbB-3 and ErbB-4 receptors, but not to the ErbB-2 receptor. However, ErbB-2 is required for signalling, and 35 heterodimers containing ErbB-2 in combination with ErbB-3 or ErbB-4 bind heregulins with higher affinity than homodimers containing ErbB-3 or ErbB-4. Plowman et al., *Nature* 366:473-75 (1993); Sliwkowski et al., *J. Biol. Chem.* 269:14661-65 (1994).

The biological activities of heregulins have been investigated by several groups. For example, Holmes et al. (*supra*) found that heregulin exerts a mitogenic effect on mammary cell lines (such as SK-BR-3 and MCF-7). Lewis et al. reported that heregulin- $\beta$ 1 stimulated proliferation and enhanced colony formation in soft agar in a number of human breast and ovarian tumor cell lines. Lewis et al., *Cancer Research* 56:1457-65 (1996). These researchers also showed that ErbB-2 is a critical mediator of heregulin responsiveness.

Pinkas-Kramarski et al. found that NDF (rat heregulin) is expressed in neurons and glial cells in embryonic and adult rat brain and primary cultures of rat brain cells, and suggested that NDF may act as a survival and maturation factor for astrocytes. Pinkas-Kramarski et al., *PNAS USA* 91:9387-91 (1994). Danilenko et al. reported that the interaction of NDF and the ErbB-2 receptor is important in directing epidermal migration and differentiation during wound repair. Danilenko et al., Abstract 3101, *FASEB* 8(4-5):A535 (1994).

Meyer and Birchmeier analyzed expression of mouse heregulin during embryogenesis and in the perinatal animal using *in situ* hybridization and RNase protection experiments. Meyer and Birchmeier, *PNAS USA* 91:1064-68 (1994). These authors conclude, based on expression of this molecule, that heregulin plays a role *in vivo* as a mesenchymal and neuronal factor. Their findings also indicated that heregulin functions in the development of epithelia.

Falls et al. (*supra*) found that chicken ARIA plays a role in myotube differentiation, namely affecting the synthesis and concentration of neurotransmitter receptors in the postsynaptic muscle cells of motor neurons. Corfas and Fischbach demonstrated that ARIA

also increases the number of sodium channels in chick muscle. Corfas and Fischbach, *J. Neuroscience* 13:2118-25 (1993).

Bovine GGFs have been reported to be mitogenic for 5 Schwann cells. See, e.g., Brockes *et al.*, *J. Biol. Chem.* 255:8374-77 (1980); Lemke and Brockes, *J. Neurosci.* 4:75-83 (1984); Brockes *et al.*, *J. Neuroscience* 4:75-83 (1984); Brockes *et al.*, *Ann. Neurol.* 20:317-22 (1986); Brockes, *Methods in Enzym.* 10 147:217-225 (1987); Marchionni *et al.*, *supra*. Schwann cells provide myelin sheathing around the axons of myelinated neurons and thus play an important role in the development, function and regeneration of peripheral nerves. The implications of this role from 15 a therapeutic standpoint have been addressed by Levi *et al.*, *J. Neuroscience* 14:1309-19 (1994). Levi *et al.* discussed the potential for construction of a cellular prosthesis including Schwann cells that could be transplanted into areas of damaged spinal cord.

20 Methods for culturing Schwann cells *ex vivo* have been described. See WO 94/00140; Li *et al.*, *J. Neuroscience* 16:2012-19 (1996).

GGFII has been shown to be mitogenic for 25 subconfluent quiescent human myoblasts, and differentiation of clonal human myoblasts in the continuous presence of GGFII results in greater numbers of myotubes after six days of differentiation. Sklar *et al.*, *J. Cell Biochem.*, Abst. W462, 18D, 540 (1994); see also WO 94/26298.

30 The relationship between the structure and function of new proteins can be investigated using any of a variety of available mutational analysis techniques. Examples of such techniques include alanine scanning mutagenesis and phagemid display.

35 Alanine scanning can be used to identify active residues (i.e., residues that have a significant effect on protein function) in a protein or protein domain.

For example, Cunningham and Wells used alanine scanning to identify residues in human growth hormone that were important for binding its receptor. Cunningham and Wells, *Science* 244:1081-85 (1989). In alanine scanning, a gene encoding the protein or domain to be scanned is inserted into an expression vector, and mutagenesis is carried out to generate a series of vectors that encode proteins or domains in which sequential residues are converted to alanine. The encoded proteins or domain are expressed from these vectors, and the activities of the alanine-substituted variants are then tested to identify those with altered activity. An alteration in activity indicates that the residue at the alanine-substituted position is an active residue.

Phagemid display was developed to allow the screening of a large number of variant polypeptides for a particular binding activity. Smith and Parmley demonstrated that foreign peptides can be "displayed" efficiently on the surface of filamentous phage by inserting short gene fragments into gene III of the fd phage. Smith, *Science* 228:1315-17 (1985); Parmley and Smith, *Gene* 73:305-18 (1985). The gene III coat protein is present in about five copies at one end of the phage particle. The modified phage were termed "fusion phage" because they displayed the foreign peptides fused to the gene III coat protein. As each fusion phage particle displayed approximately five copies of the fusion protein, this mode of phage display was termed "polyvalent display."

Scott et al. and Cwirla et al. showed that fusion phage libraries could be screened by sequential affinity selections known as "panning." Scott et al., *Science* 249:386-90 (1990); Cwirla et al., *PNAS USA* 87:6378-82 (1990). However, early efforts to select high affinity fusion phage failed, presumably due to the polyvalence of the phage particles. This problem

was solved with the development of a "monovalent" phage display system in which the fusion protein is expressed at a low level from a phagemid and a helper phage provides a large excess of wild-type coat protein.

5 Bass et al., *Proteins* 8:309-14 (1990); Lowman et al., *Biochem.* 30:10832-38 (1991). Monovalent phage display can be used to generate and screen a large number of variant polypeptides to isolate those that bind with high affinity to a target of interest.

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#### SUMMARY OF THE INVENTION

The present invention provides a heregulin variant having an amino acid sequence not found in nature and the ability to bind an ErbB receptor. In 15 one embodiment, the variant has an amino acid substitution at a selected residue corresponding to a residue of 645-amino acid native human heregulin- $\beta$ 1 selected from the group consisting of:

20 S177, H178, L179, V180, K181, E184, E186,  
K187, T188, V191, N192, G193, G194, E195,  
M198, V199, K200, D201, N204, P205, S206,  
R207, Y208, L209, K211, P213, N214, E215,  
T217, G218, D219, Q222, N223, Y224, S228, and  
F229.

25 In a variation of this embodiment, the amino acid substitution is not a replacement of the selected residue with an epidermal growth factor (EGF) residue corresponding to the selected residue.

The heregulin variant can be a variant of any 30 member of the heregulin family from any species. In one embodiment, the heregulin variant is a variant of a human heregulin, such as, for example, human heregulin- $\beta$ 1. The invention provides a human heregulin- $\beta$ 1 variant including an amino acid 35 substitution selected from the group consisting of:

S177W; H178S, E, R, or A; V180Q, I, or E;  
K181P or A; A183G; E184V, W, K, R, G, or N;

K185E, S, Q, or G; E186R; K187E or A; T188Q; E195Q; F197Y; M198R or K; K200R; D201T or I; P205T or Y; S206K, H, G, P, or R; R207Y; Y208R or L; L209M or G; K211R; P213S, T, N, or K; N214L, K, S, or E; F216M; N223H or W; and M226I.

In a variation of this embodiment, the heregulin variant includes sets of amino acid substitutions selected from this group. Some heregulin variants of the invention having sets of amino acid substitutions exhibit at least a 50-fold increase in ErbB-3 receptor affinity, which is also accompanied by an increase in ErbB-4 receptor affinity.

The invention also includes a heregulin variant that has a greater specificity for the ErbB-4 receptor, relative to the ErbB-3 receptor, than the heregulin from which the heregulin variant is derived. In one embodiment, this heregulin variant has an amino acid substitution at a selected residue corresponding to a residue of 645-amino acid native human heregulin- $\beta$ 1 selected from the group consisting of H178, L179, and R207.

In another embodiment, a heregulin variant having a greater specificity for the ErbB-4 receptor, relative to the ErbB-3 receptor, has a deletion of amino acid residues corresponding to residues S228 to K231 of 645-amino acid native human heregulin- $\beta$ 1 and a substitution of a single methionine for the deleted residues.

In addition to including one or more of the mutations disclosed herein, the heregulin variant can have one or more other modifications, such as an amino acid substitution, an insertion of at least one amino acid, a deletion of at least one amino acid, or a chemical modification. For example, the invention provides a heregulin variant that is a fragment. In a variation of this embodiment, the fragment includes

residues corresponding to a portion of human heregulin- $\beta$ 1 extending from about residue 175 to about residue 230 (i.e., the EGF-like domain). In a further variation of this embodiment, the fragment includes 5 residues corresponding to a portion of human heregulin- $\beta$ 1 extending from about residue 175 to about residue 245.

One aspect of the invention is a method for producing such a modified heregulin variant. The 10 modification(s) is selected so that the modified heregulin variant retains the ability to an ErbB receptor.

In addition to a heregulin variant, the invention provides a related nucleic acid molecule, vector, and 15 host cell. The invention also provides a method of producing a heregulin variant in which a host cell containing an expression vector capable of expressing the heregulin variant is cultured under conditions that allow expression of the heregulin variant, and the 20 heregulin variant then recovered from the culture.

Other aspects of the invention relate to various uses of a heregulin variant. For example, the invention provides a method for activating an ErbB receptor in which the heregulin variant is contacted 25 with a cell that expresses an ErbB receptor. The heregulin variant can be contacted with cells in culture, for example, to promote ex vivo survival, proliferation, or differentiation of cells, such as glial, Schwann, or muscle cells.

30 Alternatively, the heregulin variant can be combined with a pharmaceutically acceptable carrier and used to treat one of a wide range of cancers as well as diseases and disorders affecting the nervous system, musculature, and epithelia. Thus, the present 35 invention provides a pharmaceutical composition and a treatment method.

The invention also includes a method of determining whether a sample contains an ErbB receptor that binds a heregulin. In particular, a heregulin variant is contacted with a sample, and specific binding between the heregulin variant and a component of the sample is determined as an indication of the presence and/or amount of ErbB receptor(s) present in the sample.

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#### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows an alignment between the amino acid sequences in the EGF-like domains of a number of heregulin polypeptides and the amino acid sequence of the human heregulin- $\beta$ 1 EGF-like domain ("beta1"). The aligned sequences are as follows: human heregulin- $\alpha$  (alpha), human heregulin- $\beta$ 2 and - $\beta$ 3 (beta2 and beta3), neu differentiation factors a2 and b1 to b4 (ndfa2 and ndfb1-4), glial growth factor II (ggf), sensory and motor neuron-derived factor (smdf), human heregulin- $\gamma$ , and acetylcholine receptor inducing activity polypeptide (aria). The number shown for each sequence is the residue number of the first amino acid shown, as numbered from the N-terminus of the native polypeptide whose sequence is shown. "#" indicates the differences between the  $\alpha$ - and  $\beta$ -type EGF-like domains.

Figure 2 shows the results of an alanine scan of the heregulin- $\beta$ 1 EGF-like domain (heregulin- $\beta$ 1 residues 177-228). Individual amino acids in this domain were mutated to alanine and displayed monovalently on phage as gIII fusion proteins, as described in Example 2. The histogram shows the change in binding affinity of each alanine variant for ErbB-3 and ErbB-4 receptor-Ig fusions (ErbB-3-Ig and ErbB-4-Ig), as measured by phage ELISA. The X axis lists each amino acid that was changed to alanine and its position. The Y axis is the ratio of the EC<sub>50</sub> for each variant to the EC<sub>50</sub> for the wild-type heregulin- $\beta$ 1 EGF-like domain, also displayed

on phage. The EC<sub>50</sub> was calculated as the concentration of soluble receptor fusion required to displace 50% of the total amount of phage bound to immobilized receptor fusion. ErbB-3 binding results are shown with black bars, and ErbB-4 binding results are shown with white bars.

Figure 3 shows the amino acids selected for binding to ErbB-3-Ig at each position in the heregulin- $\beta$ 1 EGF-like domain (heregulin- $\beta$ 1 residues 177-228) randomized in the phage display studies described in Example 3. The length of the bars indicates the frequency of occurrence of a particular amino acid at each position in the variants from phage display libraries A-E and G-I for which sequences were determined (i.e., a longer bar indicates a higher frequency). Twelve clones were sequenced from each library, although in library H, only one clone of the twelve represented a variant having mutations in the desired randomization window (see Example 3). "WT" indicates the wild-type amino acid sequence of the heregulin- $\beta$ 1 EGF-like domain.

Figure 4 shows the amino acid substitutions in the EGF-like domains of combination variants described in Example 3. The amino acid sequence of the wild-type heregulin- $\beta$ 1 EGF-like domain (HRG8), a variant of this domain containing a deletion of heregulin- $\beta$ 1 residues 202-204 (HRG63), and the analogous domain in EGF are shown on top. The residue numbering for the portion of the heregulin- $\beta$ 1 amino acid sequence shown is indicated above this sequence (numbered from the N-terminus of native human heregulin- $\beta$ 1). The residue numbering for the portion of the EGF amino acid sequence shown is indicated below this sequence (numbered from the N-terminus of native human EGF). A " ." indicates a residue that is identical to the wild-type residue at the particular position. A "--" indicates the absence of a residue.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides heregulin variants having one or more amino acid substitutions at selected residues. Included within the scope of the invention  
5 are variants of human heregulins, and, in particular, variants of human heregulin- $\beta$ 1. A heregulin variant according to the invention can have a single amino acid substitution at a selected residue or combinations of such substitutions.

10 In addition to the amino acid substitutions specified herein, heregulin variants according to the invention can have further modifications, including, for example, deletions of amino acids. In one embodiment, a heregulin variant has N- and C-terminal  
15 deletions, leaving only amino acids corresponding to "the minimal EGF-like domain," which is sufficient for binding and activation of an ErbB receptor.

A heregulin variant of the invention is capable of binding an ErbB receptor, such as ErbB-3 or ErbB-4. In one embodiment, the variant has an enhanced affinity  
20 for an ErbB receptor compared to the affinity of the most homologous native heregulin. In addition to ErbB receptor binding, the heregulin variant can possess one or more other biological activities of a native  
25 heregulin.

The invention also provides nucleic acid molecules, vectors, and host cells related to the heregulin variants. A nucleic acid molecule of the invention encodes, or is complementary to a nucleic  
30 acid molecule encoding, a heregulin variant of the invention or a fragment thereof. The nucleic acid molecule can be double- or single-stranded DNA or RNA. A nucleic acid molecule of the invention can be inserted into an appropriate vector for propagation  
35 and/or expression of an encoded heregulin variant. Such vectors are introduced into suitable hosts, for

example, to allow recombinant production of a heregulin variant.

The heregulin variants of the invention are useful in a variety of therapeutic and non-therapeutic applications. In particular, heregulin variants can be used in treating cancer and various diseases and disorders of the nervous system, musculature, and epithelia. Accordingly, the invention encompasses a pharmaceutical composition including a heregulin variant and related treatment methods.

Heregulin variants can also be employed in a variety of non-therapeutic applications, such as cell culture methods and diagnostic methods. For example, heregulin variants can be used to promote the ex vivo survival, proliferation, or differentiation of cells, including glial and muscle cells. In an exemplary diagnostic application, heregulin variants are employed in the diagnosis of a cancer characterized by erbB (e.g., erbB2) overexpression. Accordingly, the invention also includes kits useful in practicing the above-described methods.

#### Definitions

As used herein, the following words or phrases have the definitions indicated below, unless otherwise indicated.

The terms "amino acid" and "residue" are used interchangeably herein.

The term "wild-type amino acid" or "wild-type residue" means the amino acid present at a given position(s) in a native polypeptide.

Amino acids are denoted herein by the standard three-letter or one-letter code.

Residues in two or more polypeptides are said to "correspond" if the residues occupy an analogous position in the polypeptide structures. As is well known in the art, analogous positions in two or more

polypeptides can be determined by aligning the polypeptide sequences based on amino acid sequence or structural similarities. Those skilled in the art understand that it may be necessary to introduce gaps 5 in either sequence to produce a satisfactory alignment. For example, residues in human EGF that correspond to residues in human heregulin- $\beta$ 1 are shown in an alignment between the amino acid sequence of the heregulin- $\beta$ 1 EGF-like domain (heregulin- $\beta$ 1 residues 10 177-228) and the analogous EGF domain (EGF residues 1-48) in Figure 4.

Residues in two or more heregulins are said to "correspond" if the residues are aligned in the best sequence alignment. The "best sequence alignment" 15 between two polypeptides is defined as the alignment that produces the largest number of aligned identical residues. The best sequence alignment for a number of heregulin polypeptides is shown in Figure 1.

Residue positions in heregulin- $\beta$ 1 are designated 20 herein by the three-letter or one-letter code for the amino acid, followed by the position number, as numbered from the N-terminus of native human pro-heregulin- $\beta$ 1 (which is 645 amino acids in length). E.g., the serine at position 177 of heregulin- $\beta$ 1 is 25 denoted "Ser177" or "S177."

Hereinafter, unless otherwise indicated, residue positions in a heregulin, heregulin variant, or related protein, such as EGF, are specified herein with reference to the amino acid numbering of native human 30 heregulin- $\beta$ 1. For example, a heregulin- $\beta$ 1 variant can have a N-terminal deletion of residues 1-176. The first amino acid in this variant is identified herein as "the residue corresponding to Ser177 of 645-amino acid human heregulin- $\beta$ 1" because the first residue of 35 the heregulin variant and Ser177 of heregulin- $\beta$ 1 are aligned in the best alignment between the two polypeptides.

Example 3 discloses heregulin- $\beta_1$  variants containing residues corresponding to residues 177 to 228 of heregulin- $\beta_1$ , which is termed "the minimal EGF-like domain." For these variants, residue numbers 5 also are expressed, in parentheses, in terms of the position of the residue in the minimal EGF-like domain (hereinafter "heregulin- $\beta_1$  EGF" or "HRG- $\beta_1$  EGF"), i.e., residues 1-52. Residue positions numbered according to native human heregulin- $\beta_1$  can be converted to residue 10 positions in the minimal EGF-like domain by subtracting 176 from the former position number. E.g., for heregulin- $\beta_1$  Ser177, subtracting 176 from 177 gives 1, and thus heregulin- $\beta_1$  EGF Ser1 identifies the same 15 position as heregulin- $\beta_1$  Ser177. The same numbering system is used in Example 4.

Amino acid substitutions are indicated by listing the residue position followed by the code for the amino acid substituted into the heregulin polypeptide. Thus, 20 a substitution of alanine at Ser177 of heregulin- $\beta_1$  is expressed as "heregulin- $\beta_1$  Ser177Ala," "Ser177Ala", or "S177A." In this example, serine is the "replaced amino acid," and alanine is the "replacement amino acid."

As used to describe two amino acid sequences, the 25 term "homologous" indicates that the amino acid sequences have some degree of amino acid sequence identity.

#### Heregulin Variants

30 The present invention includes a heregulin variant. The term "heregulin variant" means a polypeptide variant of a native heregulin. A native heregulin is defined as a polypeptide having the full-length amino acid sequence of any of the family of 35 naturally occurring heregulin polypeptides. This family encompasses pro-heregulins as well as the

soluble forms of these proteins. The invention is exemplified with variants of human heregulin- $\beta$ 1. See Examples 1-3. However, the heregulin family encompasses any naturally occurring polypeptide having an EGF-like domain that has at least 70 percent sequence identity with the EGF-like domain of heregulin- $\beta$ 1 when these domains are aligned in the best alignment. Thus, a native heregulin can be from any species and one of a number of naturally occurring isoforms or allelic forms. Exemplary heregulin polypeptides include neu differentiation factors, glial growth factors, sensory and motor neuron-derived factor, and acetylcholine receptor inducing activity polypeptide.

In one embodiment, the heregulin variant is a variant of a mammalian heregulin. In a variation of this embodiment, the heregulin variant is a variant of a human heregulin. Examples of human heregulins include heregulin- $\alpha$  (HRG- $\alpha$ ), heregulin- $\beta$ 1 (HRG- $\beta$ 1), heregulin- $\beta$ 2 (HRG- $\beta$ 2), heregulin- $\beta$ 3 (HRG- $\beta$ 3), and heregulin- $\gamma$  (HRG- $\gamma$ ).

A heregulin variant according to the invention has an amino acid sequence not found in nature in which a wild-type residue in a native heregulin is replaced with a different residue. This amino acid substitution is at one or more selected residues corresponding to a residue of native human heregulin- $\beta$ 1. The selected residue(s) is chosen from the following group:

S177, H178, L179, V180, K181, E184, E186,  
30 K187, T188, V191, N192, G193, G194, E195,  
M198, V199, K200, D201, N204, P205, S206,  
R207, Y208, L209, K211, P213, N214, E215,  
T217, G218, D219, Q222, N223, Y224, S228, and  
F229.

35 In one embodiment, however, the amino acid substitution is not a replacement of the selected residue with an EGF residue corresponding to the selected residue.

Substitution of any of the above residues in heregulin- $\beta 1$  with alanine has at least a two-fold effect on affinity for the ErbB-3 or ErbB-4 receptors, as determined by phage ELISA. See Example 2.

5 In one embodiment, the selected residue is chosen from the following group:

S177, H178, L179, E186, K187, T188, V191,  
N192, G193, G194, E195, R207, L209, K211,  
P213, N214, T217, G218, Q222, Y224, and F229.

10 Substitution of the any of these residues in heregulin- $\beta 1$  with alanine has at least a five-fold effect on affinity for the ErbB-3 or ErbB-4 receptors, as determined by phage ELISA. See Example 2.

15 In a variation of this embodiment, the selected residue is chosen from the following group:

H178, L179, K187, N192, G193, G194, E195,  
R207, K211, T217, G218, Q222, and Y224.

20 Substitution of the any of these residues in heregulin- $\beta 1$  with alanine has at least a 10-fold effect on affinity for the ErbB-3 or ErbB-4 receptors, as determined by phage ELISA. See Example 2.

Generally, if function is to be preserved at a position selected for substitution, the residue used to replace the selected residue is not substantially different in character from the wild-type residue, i.e., the amino acid substitution is a conservative substitution. Amino acids can be grouped according to character as shown in Table 1.

Table 1  
*Groups of Amino Acids  
 Having Similar Character*

5	<u>Group</u>	<u>Character</u>	<u>Amino Acids</u>
	a	positively charged	Lys, Arg, His
	b	negatively charged	Asp, Glu
	c	amide	Asn, Gln
	d	aromatic	Phe, Tyr, Trp
10	e	hydrophobic	Pro, Gly, Ala, Val, Leu, Ile, Met
	f	uncharged hydrophilic	Ser, Thr

To preserve function, therefore, the residue used to replace the wild-type residue is usually selected from the same group or a related group. In addition, serine or alanine can be used to replace most other residues. Table 2 shows conservative substitutions for each amino acid, identifying related groups for each and indicating which amino acids can be replaced with serine or alanine. Table 2 also shows preferred amino acid substitutions.

Table 2  
Conservative Amino Acid Substitutions

		<u>Replacement Amino Acid Selected From</u>	<u>Preferred Substitutions</u>
5	AA:		
10	Ala	e*: Pro, Gly, Ala, Val, Leu, Ile, Met	Ser
		f: Ser, Thr	
	Arg	a: Lys, Arg, His	Lys
		Ser, Ala	Ser, Ala
	Asn	a: Lys, Arg, His	Gln
		c: Asn, Gln	
15		Ser, Ala	Ser, Ala
	Asp	b: Asp, Glu	Glu
		c: Asn, Gln	
		Ser, Ala	
20	Cys	e: Pro, Gly, Ala, Val, Leu, Ile, Met	Ser, Ala
		f: Ser, Thr	Ala
	Gln	a: Lys, Arg, His	Ser
		c: Asn, Gln	Asn
		Ser, Ala	Ser, Ala
25	Glu	b: Asp, Glu	Asp
		c: Asn, Gln	
		Ser, Ala	Ser, Ala
	Gly	e: Pro, Gly, Ala, Val, Leu, Ile, Met	Pro, Ala
		f: Ser, Thr	
30	His	a: Lys, Arg, His	Arg
		Ser, Ala	Ser, Ala
	Ile	e: Pro, Gly, Ala, Val, Leu, Met	Ala, Val, Leu
	Leu	e: Pro, Gly, Ala, Val, Ile, Met	Ala, Val, Ile
	Lys	a: Lys, Arg, His	Arg
		Ser, Ala	Ser, Ala
35	Met	e: Pro, Gly, Ala, Val, Leu, Ile, Met	Ala, Val, Leu, Ile
	Phe	a: Lys, Arg, His	
		d: Phe, Tyr, Trp	Tyr
		Ala, Val, Leu, Ile	Ala, Val, Leu, Ile
40	Pro	a: Lys, Arg, His	Phe
		d: Phe, Tyr, Trp	Gly, Ala
		Gly, Ala	Thr
	Ser	a: Lys, Arg, His	
		f: Ser, Thr	
		Ala	Ala
45	Thr	a: Lys, Arg, His	
		f: Ser, Thr	Ser
		Ala	Ala
	Trp	d: Phe, Tyr, Trp	Phe
		Ala	Ala
50	Tyr	d: Phe, Tyr, Trp	Phe,
		Ala, Val, Leu, Ile	Ala, Val, Leu, Ile
	Val	e: Pro, Gly, Ala, Val, Leu, Ile, Met	Leu, Ile,
		Ser, Ala	Ser, Ala

55 \* Wild-type amino acid.

\* Lower-case letters refer to the groups of amino acids in Table 1.

In one embodiment, the heregulin variant is a variant of human heregulin- $\beta$ 1 and includes an amino acid substitution(s) chosen from the following group:

S177W; H178S, E, R, or A; V180Q, I, or E;  
5 K181P or A; A183G, T, or D; E184V, W, K, R,  
G, or N; K185E, S, Q, or G; E186R; K187E or  
A; T188Q; E195Q; F197Y; M198R or K; K200R;  
D201T or I; P205T or Y; S206K, H, G, P, or R;  
R207Y; Y208R or L; L209M or G; K211R; P213S,  
10 T, N, or K; N214L, K, S, or E; F216M; N223H  
or W; and M226I.

Another aspect of the invention is a variant of human heregulin- $\beta$ 1 including a set of amino acid substitutions, such as any of the heregulin variants 15 described in Example 3. The set of amino acid substitutions is chosen from the group indicated below (the variant number from Example 3 is shown in the left-hand column, followed by the set of amino acid substitutions for that variant):

20 B5: A183G, E184W, K185D, E186R, K187E, T188G,  
M226I;  
B10: A183D, E184K, K185S, E186R, K187E, T188G,  
M226I;  
D1: F197Y, M198K, K200R, D201I, M226I;  
25 E2: P205Y, S206G, R207Y, Y208L, L209M;  
E3: P205Y, S206R, R207Y, Y208R, L209M, M226I;  
E6: P205T, S206H, R207Y, Y208R, L209M;  
E8: P205T, S206K, R207Y, Y208R, L209G;  
I1: N223W, M226I;  
30 I2: N223H, M226I;  
HRG37: S177W, H178E, K181P, A183G, E184W, K185D,  
E186R, K187E, T188G, M226I;  
HPG48: P205Y, S206G, R207Y, Y208L, L209M, M226I;  
HRG53: A183G, K185E, E186R, K187E, T188G, F197Y,  
35 M198R, D201T;  
HRG54: A183G, K185E, E186R, K187E, T188G, P205Y,  
S206G, R207Y, Y208L, L209M;

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HRG55: A183G, K185E, E186R, K187E, T188G, F197Y,  
M198R, D201T, P205Y, S206G, R207Y, Y208L,  
L209M;  
HRG56: A183G, K185E, E186R, K187E, T188G, M226I;  
5 HRG57: F197Y, M198R, D201T, P205Y, S206G, R207Y,  
Y208L, L209M;  
HRG58: F197Y, M198R, D201T, P205Y, S206G, R207Y,  
Y208L, L209M, M226I;  
HRG59: F197Y, M198R, D201T, M226I;  
10 HRG60: A183G, K185E, E186R, K187E, T188G, F197Y,  
M198R, D201T, M226I;  
HRG61: A183G, K185E, E186R, K187E, T188G, P205Y,  
S206G, R207Y, Y208L, L209M, M226I;  
HRG62: A183G, K185E, E186R, K187E, T188G, F197Y,  
15 M198R, D201T, P205Y, S206G, R207Y, Y208L,  
L209M, M226I;  
HRG71: F197Y, M198R, D201T, P205Y, S206G, R207Y,  
Y208L, L209M, N223H, M226I; and  
HRG73: A183G, K185E, E186R, K187E, T188G, F197Y,  
20 M198R, D201T, P205Y, S206G, R207Y, Y208L,  
L209M, N223H, M226I.

Each of these sets of amino acid substitutions produces  
at least a five-fold increase in ErbB-3 receptor  
affinity, as determined by phage ELISA. See Example 3.  
25 In a variation of this embodiment, the set of  
amino acid substitutions is chosen from the following  
group:

B5: A183G, E184W, K185D, E186R, K187E, T188G,  
M226I;  
30 E2: P205Y, S206G, R207Y, Y208L, L209M;  
I2: N223H, M226I;  
HRG48: P205Y, S206G, R207Y, Y208L, L209M, M226I;  
HRG53: A183G, K185E, E186R, K187E, T188G, F197Y,  
M198R, D201T;  
35 HRG56: A183G, K185E, E186R, K187E, T188G, M226I;  
HRG57: F197Y, M198R, D201T, P205Y, S206G, R207Y,  
Y208L, L209M;

HRG58: F197Y, M198R, D201T, P205Y, S206G, R207Y,  
Y208L, I209M, M226I;  
HRG59: F197Y, M198R, D201T, M226I;  
HRG60: A183G, K185E, E186R, K187E, T188G, F197Y,  
5 M198R, D201T, M226I;  
HRG61: A183G, K185E, E186R, K187E, T188G, P205Y,  
S206G, R207Y, Y208L, L209M, M226I;  
HRG62: A183G, K185E, E186R, K187E, T188G, F197Y,  
M198R, D201T, P205Y, S206G, R207Y, Y208L,  
10 L209M, M226I;  
HRG71: F197Y, M198R, D201T, P205Y, S206G, R207Y,  
Y208L, L209M, N223H, M226I; and  
HRG73: A183G, K185E, E186R, K187E, T188G, F197Y,  
M198R, D201T, P205Y, S206G, R207Y, Y208L,  
15 L209M, N223H, M226I.

Each of these sets of amino acid substitutions produces at least a 20-fold increase in ErbB-3 receptor affinity, as determined by phage ELISA. See Example 3.

In another variation of this embodiment, the set 20 of amino acid substitutions is chosen from the following group:

HRG58: F197Y, M198R, D201T, P205Y, S206G, R207Y,  
Y208L, L209M, M226I;  
HRG60: A183G, K185E, E186R, K187E, T188G, F197Y,  
25 M198R, D201T, M226I;  
HRG71: F197Y, M198R, D201T, P205Y, S206G, R207Y,  
Y208L, L209M, N223H, M226I; and  
HRG73: A183G, K185E, E186R, K187E, T188G, F197Y,  
M198R, D201T, P205Y, S206G, R207Y, Y208L,  
30 L209M, N223H, M226I.

Each of these sets of amino acid substitutions produces at least a 50-fold increase in ErbB-3 receptor affinity, as determined by phage ELISA. See Example 3.

The invention also includes a heregulin variant 35 that has a greater specificity for the ErbB-4 receptor, relative to the ErbB-3 receptor, than the heregulin from which the heregulin variant is derived. Such

enhanced ErbB-4 receptor specificity can be measured, for example, as a lower variant:wild-type EC<sub>50</sub> ratio for binding to the ErbB-4 receptor than for binding to ErbB-3 receptor. Generally, a heregulin variant having enhanced ErbB-4 receptor specificity has approximately wild-type affinity for the ErbB-4 receptor or better together with a significantly reduced (i.e., at least about 5-10-fold) affinity for the ErbB-3 receptor.

In one embodiment, a heregulin variant having enhanced ErbB-4 receptor specificity has an amino acid substitution at a selected residue corresponding to a residue of 645-amino acid native human heregulin- $\beta$ 1 selected from the group consisting of H178, L179, and R207. For example, the invention provides a human heregulin- $\beta$ 1 variant including the amino acid substitution H178E or R207P.

In another embodiment, a heregulin variant having enhanced ErbB-4 receptor specificity has a deletion of amino acid residues corresponding to residues S228 to K231 of 645-amino acid native human heregulin- $\beta$ 1 and a substitution of a single methionine for the deleted residues. In a variation of this embodiment, the heregulin variant also includes the amino acid substitution H178L.

In addition to the above amino acid substitutions, the heregulin variant can optionally have any of the following modifications, singly or in combination:

- (1) one or more additional amino acid substitutions;
- (2) one or more amino acids added to the N- or C-terminus of, or inserted within, the amino acid sequence of the heregulin variant;
- (3) one or more amino acids deleted from the heregulin variant; and
- (4) one or more covalent modifications of an amino acid in the heregulin variant.

Thus, the heregulin variant can be "substantially full-length," which, as used herein, means that the heregulin variant is at least 90% as long as the native

heregulin to which the variant is most homologous. Alternatively, the heregulin variant can be a "fragment" that is less than 90% as long as the most homologous native heregulin. Heregulin variants that 5 are fragments are usually about 30 to about 100 amino acids, more usually about 40 to about 60 amino acids, even more usually about 45 to about 65 amino acids, and most usually about 50 amino acids in length.

For example, the heregulin variant can include 10 amino acids corresponding to "the minimal EGF-like domain." The minimal EGF-like domain is a portion of a native heregulin that is sufficient for binding and activation of an ErbB receptor. In general, the minimal EGF-like domain is less than about 70 amino 15 acids and usually less than about 60 amino acids in length. As used herein with reference to human heregulin- $\beta$ 1, the minimal EGF-like domain extends from residues 177-228. Unless otherwise indicated, "HRG- $\beta$ 1 EGF" refers to the minimal EGF-like domain.

Examples of suitable covalent modifications of a heregulin variant according to the invention include, but are not limited to, conjugation with a detectable label, "pegylation," and conjugation with a cytotoxic agent. A heregulin variant can be conjugated to any of 25 a wide variety of available labels to produce a conjugate useful for detecting the presence of ErbB receptors in a sample. Suitable labels include a radioisotope, a fluorescent label, and an enzyme label. Exemplary radioisotope labels are  $^{35}$ S,  $^{14}$ C,  $^{125}$ I,  $^3$ H, and 30  $^{131}$ I. Heregulin variants can be conjugated to radioisotopes as described generally in Current Protocols in Immunology Vols. 1 & 2 (Coligan et al. ed., Wiley Publishers).

Fluorescent labels suitable for conjugation to a 35 heregulin variant include a rare earth chelate (a europium chelate), fluorescein, rhodamine, dansyl, Lissamine, phycoerythrin, and Texas Red, and

derivatives thereof. Conjugates can be prepared as described, for example, in Current Protocols in Immunology *supra*.

Various enzyme-substrate systems are available, 5 and U.S. Patent No. 4,275,149 provides a review of some of these. In general, enzymes useful in such systems catalyze a readily detectable chemical alteration of a substrate. For example, the enzyme can catalyze a color change, which can be measured spectrophotometrically, or a change in fluorescence or chemiluminescence, which can be detected using a fluorometer or chemiluminometer, respectively. 10 Exemplary enzyme labels include a luciferase, malate dehydrogenase, urease, a peroxidase, alkaline phosphatase,  $\beta$ -galactosidase, glucoamylase, lysozyme, a saccharide oxidase, a heterocyclic oxidase, lactoperoxidase, microperoxidase, and the like. 15 Heregulin variants can be conjugated to enzyme labels as described generally in O'Sullivan et al., *Methods in Enzym.* 73:47-166 (1981), and in Current Protocols in Immunology (*supra*). Suitable substrates for use with a given enzyme label are well known to those skilled in the art. 20

Another exemplary modification of a heregulin 25 variant of the invention is pegylation, which refers to the conjugation of one or more polyethylene glycol (PEG) groups to the  $\epsilon$ -amino group(s) of a polypeptide. PEGylation may be desired when the heregulin variant is intended for pharmaceutical use, as pegylation can 30 increase *in vivo* half-life and/or reduce immunogenicity and potential toxicity of therapeutic proteins. See, e.g., Abuchowski et al., *J. Biol. Chem.* 252:3582-86 (1977).

Conjugation of a heregulin variant with a 35 cytotoxic agent produces a targeted cytotoxic agent that specifically binds cells expressing appropriate ErbB receptors on their surface. The term "cytotoxic

"agent" refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term includes, for example, a radioactive isotope (e.g., I, Y, Pr) and a chemotherapeutic agent.

5 A "chemotherapeutic agent" is defined herein as any chemical compound useful in the treatment of cancer. The term "cancer" refers to the physiological condition in mammals that is characterized by unregulated cell growth. Examples of cancer include  
10 but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia. More particular examples of such cancers include squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, gastric cancer, pancreatic cancer, glial cell tumors such as  
15 glioblastoma and neurofibromatosis, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, renal cancer, prostate cancer, vulval cancer,  
20 thyroid cancer, hepatic carcinoma and various types of head and neck cancer. Examples of chemotherapeutic agents include Adriamycin, Doxorubicin, 5-Fluorouracil (5-FU), Cytosine arabinoside (Ara-C), Cyclophosphamide, Thiotepa, Busulfan, Cytoxin, Taxol, Methotrexate,  
25 Cisplatin, Melphalan, Vinblastine, Bleomycin, Etoposide, Ifosfamide, Mitomycin C, Mitoxantrone, Vincristine, VP-16, Vinorelbine, Carboplatin, Teniposide, Daunomycin, Carminomycin, Aminopterin, Dactinomycin, a Mitomycin, Nicotinamide, an  
30 Esperamicin, Melphalan and any related nitrogen mustard, and an endocrine therapeutic (such as diethylstilbestrol [DES], Tamoxifen, a leutinizing hormone releasing hormone-antagonizing drug, a progestin, an anti-progestin, etc.).

35 In addition to conjugation to a chemical compound, any of the above-described heregulin variants can be modified by fusion to a heterologous polypeptide to

produce a "chimeric heregulin variant." (Chimeric heregulin variants are also referred to herein as "fusion proteins.) Typically, the heterologous polypeptide is fused at the N- or C terminus of the 5 heregulin variant to preserve the biological activity (described further below) of the heregulin variant. However, the heterologous polypeptide can also be introduced into regions of the heregulin variant that are not critical for biological activity. Generally, 10 chimeric heregulin variants are produced by recombinant techniques. Examples of chimeric heregulin variants include a heregulin variant fused to a "signal sequence," a "purification handle" and an immunoglobulin sequence.

15 A "signal sequence" is an amino acid sequence that directs the secretion of a polypeptide fused thereto from a cell expressing the chimeric protein. Thus, fusion of a heregulin variant to a signal sequence facilitates recombinant production of the heregulin 20 variant because the chimeric heregulin variant is secreted into the host cell culture medium, from which the chimeric heregulin variant can be recovered with relative ease.

A suitable signal sequence can be obtained from 25 any protein that has a signal sequence and is typically (but not always) fused to the N-terminus of the heregulin variant. DNA encoding prokaryotic signal sequences can be obtained, for example, from *lamB* or *ompF*, *MalE*, *PhoA*, and other genes. A convenient 30 prokaryotic signal sequence for practicing the invention is the *E. coli* heat-stable enterotoxin II (STII) signal sequence.

A "purification handle" is a portion of a polypeptide that binds another polypeptide, termed a 35 "binding partner." The fusion of a purification handle to a heregulin variant confers on the variant the ability to bind the binding partner, which facilitates

purification of the resultant chimeric heregulin variant. Generally, the purification handle is selected so that the binding partner does not substantially cross-react with other components present  
5 in the mixture from which the chimeric heregulin variant is to be purified. As used herein, the term "does not substantially cross-react" means that the affinity of the binding partner for the purification handle is at least about 20-fold, usually at least  
10 about 100-fold, more usually at least about 1000-fold, any affinity for any other components present in the mixture.

In one embodiment, the purification handle is an epitope recognized by an antibody, and the chimeric heregulin variant is therefore termed an "epitope-tagged heregulin variant." Suitable epitopes generally have at least five amino acids, usually between about 10 and about 50 amino acids, and more usually between about 10 and about 30 amino acids.  
15

20 A chimeric molecule that includes a heregulin variant fused to an immunoglobulin sequence is termed "a heregulin variant immunoadhesin." In one embodiment, the immunoglobulin sequence is an immunoglobulin constant domain. The immunoglobulin sequence in a heregulin variant immunoadhesin can be obtained from IgG<sub>1</sub>, IgG<sub>2</sub>, IgG<sub>3</sub> or IgG<sub>4</sub> subtypes, IgA, IgE, IgD, or IgM. In one embodiment, the immunoglobulin sequence is obtained from IgG<sub>1</sub> or IgG<sub>3</sub>.  
25

30 Other examples of chimeric heregulin variants include heregulin variants fused to thioredoxin, a "salvage receptor binding epitope," or a cytotoxic polypeptide. Fusion of a heregulin variant with thioredoxin enhances expression and provides a purification handle that facilitates purification using phenylarsine oxide, which can be covalently bound to a solid support, such as agarose. (Agarose  
35 functionalized with phenylarsine is available

commercially as Thibond™ Resin from Invitrogen Corp., San Diego, CA.) Exemplary thioredoxin-variant fusion proteins are described in Example 2.

The term "salvage receptor binding epitope" refers 5 to an epitope of the Fc region of an IgG molecule (e.g., IgG<sub>1</sub>, IgG<sub>2</sub>, IgG<sub>3</sub>, or IgG<sub>4</sub>) that increases the in vivo serum half-life of the IgG. Salvage receptor binding epitopes suitable for fusion to a heregulin variant according the invention include any of the 10 known salvage receptor binding epitopes.

The term "cytotoxic polypeptide" refers to a polypeptide that inhibits a cellular function or kills 15 cells. Cytotoxic polypeptides suitable for fusion to a heregulin variant include an enzymatically active toxin of bacterial, fungal, plant, or animal origin and fragments thereof and an oncogene product/tyrosine kinase inhibitor, such as a peptide that inhibits binding of a tyrosine kinase to a SH2-containing substrate protein (see WO 94/07913, for example).

In one embodiment, a chimeric heregulin variant 20 includes a heregulin variant fused to an enzyme that converts a "prodrug" to an active drug. Typically, the "prodrug" is a precursor or derivative form of a cytotoxic drug that is less cytotoxic than the drug 25 itself and is capable of being enzymatically activated or converted to the cytotoxic drug. The prodrugs of this invention include, but are not limited to, a phosphate-containing prodrug, a thiophosphate-containing prodrug, a sulfate-containing prodrug, a peptide-containing prodrug, a D-amino acid-modified prodrug, a glycosylated prodrug, a  $\beta$ -lactam-containing prodrug, a phenoxyacetamide-containing prodrug, a phenylacetamide-containing prodrug, 5-fluorocytosine, a 5-fluorouridine prodrug, and derivatives thereof. 30 Examples of cytotoxic drugs that can be derivatized to produce a prodrug for use in this invention include, 35

but are not limited to, those chemotherapeutic agents described above.

A heregulin variant according to the invention is capable of binding an ErbB receptor. The term "ErbB receptor" refers to any of the mammalian class I tyrosine kinase receptors. Examples of such receptors include the ErbB-1 receptor (also known as "the EGF receptor"), the ErbB-2 receptor (also called "the HER2 receptor"), the ErbB-3 (or "HER3") receptor, and the ErbB-4 (or "HER4") receptor. The phrase "capable of binding" is used to describe a polypeptide that binds another polypeptide with a dissociation constant ( $K_d$ ) of at least 1 mM.

Exemplary heregulin variants that are capable of binding the ErbB-3 and ErbB-4 receptors are discussed above and in the examples. The production of additional heregulin variants, having further modifications (e.g., additional amino acid substitutions, additions, insertions, or deletions, or covalent modifications) and of chimeric heregulin variants is within the level of skill in the art.

Furthermore, in light of the teachings herein, those skilled in the art can design a large number of additional variants that preserve the binding activity of the heregulin variants of the invention. For example, a conservative substitution in a noncritical residue of a heregulin variant (as identified in Example 2) is not expected to significantly alter ErbB receptor binding. Moreover, any effects on ErbB receptor binding can readily be determined in a simple binding assay, such as those described in Examples 1-3. Thus, the invention encompasses all heregulin variants having amino acid substitutions at the specific positions discussed above, regardless of any additional modifications that may be present.

In addition to ErbB receptor binding, a heregulin variant of the invention can possess one or more other

biological activities of a native heregulin. For example, the heregulin variant can also have the ability to activate an ErbB receptor. The phrase "ability to activate an ErbB receptor" refers to the 5 ability to cause the intracellular kinase domain of an ErbB receptor to phosphorylate tyrosine residues. Generally, receptor activation involves binding of a heregulin to a receptor complex of two or more ErbB receptors (e.g., an ErbB-2/ErbB-3 or ErbB-2/ErbB-4 10 complex). Receptor binding activates a kinase domain of one or more of the receptors, which results in phosphorylation of tyrosine residues in one or more of the receptors and/or phosphorylation of tyrosine residues in additional substrate polypeptides(s). ErbB 15 receptor phosphorylation can be quantified using the tyrosine phosphorylation assays described in Example 3.

Furthermore, a heregulin variant of the invention can be capable of enhancing the survival, proliferation, and/or differentiation of cells having 20 suitable ErbB receptors. The phrase "enhancing survival of cells" refers to increasing the period of existence of cells, either in vitro or in vivo, relative to the period of existence of cells that have not been exposed to the heregulin variant ("untreated 25 cells").

The expression "enhancing proliferation of cells" means increasing the rate or number of mitotic divisions, either in vitro or in vivo, relative to untreated cells. An increase in cell proliferation in 30 cell culture can be detected by counting the number of cells before and after exposure to the heregulin variant or by microscopic examination of the degree of confluence. Cell proliferation can also be quantified by measuring <sup>3</sup>H-thymidine uptake by the cells.

35 The phrase "enhancing differentiation of cells" refers to increasing the extent of cell specialization. Cell specialization is characterized by the acquisition

of one or more characteristics that differ from those of the original cells. Thus, the extent of cell specialization is typically determined by screening for a change in the phenotype of the cell (e.g., 5 identifying a change in cellular morphology).

Exemplary cells that express ErbB receptors, and are therefore responsive to heregulins, include SK-BR-3 cells, glial cells, glioblastoma cells, Schwann cells, hepatocytes, epithelial cells, and muscle cells. Glial 10 cells are derived from the central nervous system and include oligodendrocytes and astrocytes. Muscle cells expressing ErbB receptors include muscle cell precursors (myoblasts) as well as the more specialized skeletal, cardiac, and smooth muscle cells.

15 Other biological activities that a heregulin variant of the invention can possess include induction of ion channel (e.g. Na<sup>+</sup> channel) formation; induction of acetylcholine receptor synthesis at the neuromuscular junction; enhancement of the formation of 20 a synaptic junction between a neuron and a muscle, nerve, or glandular cell; downregulation of estrogen receptor; and cell internalization (possibly associated with nuclear localization).

A heregulin variant is produced by any suitable 25 method, including peptide synthesis and recombinant techniques. Generally, recombinant techniques, which are described in detail below, are employed for a heregulin variant longer than about 50 or amino acids.

30 A heregulin variant having enhanced specificity for the ErbB-4 receptor, relative the ErbB-3 receptor, can be prepared by mutagenizing at one or more heregulin residues and selecting variants having enhanced ErbB-4 receptor specificity. Generally, a residue chosen for mutagenesis in this context is 35 characterized by a difference in effect on binding to the ErbB-4 receptor, as compared the effect on binding to the ErbB-3 receptor. Such residues are evident, for

instance, from the alanine-scanning data presented in Example 2.

Variants having enhanced ErbB-4 receptor specificity are selected by screening for binding to 5 ErbB-4 receptor using any suitable screening method, such as monovalent phage display, which described in Example 4. The results can be improved by subjecting variants to "counter-selection," which in this case entails the removal of variants that bind with high 10 affinity to the ErbB-3 receptor. Example 4 demonstrates that counter-selection against ErbB-3-Ig produces a significant enrichment in variants exhibiting greater specificity for ErbB-4-Ig, relative to ErbB-3-Ig, than that of wild-type HRG- $\beta$ 1.

15

#### Nucleic Acid Molecules

The present invention also includes a nucleic acid molecule related to the heregulin variant. The term "nucleic acid molecule" encompasses single-stranded and 20 double-stranded DNA molecules, including genomic DNA, cDNA, DNA produced by an amplification reaction (such as polymerase chain reaction ["PCR"]), and DNA produced by oligonucleotide synthesis, as well as RNA molecules, such as mRNA. Genomic DNA can include non-transcribed 25 and transcribed regions (such as 5' and 3' non-coding regions, introns, and heregulin variant coding regions). cDNA and mRNA molecules contain sequences corresponding to transcribed regions.

A nucleic acid molecule according to the invention 30 has a nucleotide sequence not found in nature and encodes, or is complementary to a nucleic acid molecule encoding, a heregulin variant of the invention or a fragment thereof. A complementary nucleotide sequence is capable of forming Watson-Crick bonds with its 35 complement, in which adenine pairs with thymine or uracil and guanine pairs with cytosine. A double-stranded DNA molecule encodes one of the heregulin

variants, whereas a single-stranded DNA or RNA molecule is either the coding (sense) strand or the noncoding (anti-sense) strand. When the nucleic acid molecule encodes (or is complementary to a nucleic acid molecule 5 encoding) a fragment of a heregulin variant, the fragment includes at least one amino acid substitution.

Because of the redundancy of the genetic code, there are a large number of possible nucleic acid molecules related to each heregulin variant. More 10 specifically, because several different codons encode the same amino acid, a large number of different nucleic acid molecules encode (or are complementary to a nucleic acid molecule encoding) the same heregulin variant.

Generally, a heregulin variant of the invention is produced by mutating a naturally occurring DNA sequence 15 to introduce the desired mutations into the heregulin variant amino acid sequence. However, it may also be advantageous to change one or more codons in a nucleic acid molecule without altering the encoded amino acid. Examples of such "silent mutations" within the scope of 20 the present invention include, for example, mutations that create or destroy restriction endonuclease sites to facilitate construction of a desired vector and 25 mutations that enhance expression of the encoded heregulin variant. Examples of the latter include nucleotide substitutions designed to reduce the formation of 5' stem and loop structures in the transcribed mRNA or to provide codons that are more 30 readily transcribed by the selected host (e.g., the well-known preference codons for *E. coli* or yeast expression).

A nucleic acid molecule of the invention can be incorporated into a vector (as described further below) 35 or used, for example, as a hybridization probe or an amplification primer. A hybridization probe according to the present invention is useful for detecting a

nucleic acid molecule containing a desired mutation, such as, for example, in screening bacterial transformants to identify clones containing the mutated nucleic acid molecule.

5 Such probes are generally at least about 20 nucleotides and usually less than two kilobases. The probe includes a number of nucleotides that is sufficient, under the hybridization conditions used, to hybridize with a mutated sequence to be detected and to  
10 be substantially free from hybridization with other sequences. Typically, a probe of the present invention is at least about 50 nucleotides, and usually about 100 nucleotides in length.

An amplification primer according to the invention  
15 can be used in a conventional amplification protocol, such as PCR, to detect a nucleic acid molecule containing a desired mutation or to produce sufficient amounts of such a molecule for sequencing, insertion into a vector, etc. An amplification primer is  
20 typically used as a member of a primer pair, including a 5' upstream primer that hybridizes with the 5' end of the nucleic acid sequence to be amplified and a 3' downstream primer that hybridizes with the complement of the 3' end of the sequence to be  
25 amplified.

In general, a primer according to the invention includes a number of nucleotides that is sufficient, under the hybridization conditions used, to hybridize with a mutated sequence and to be substantially free  
30 from hybridization with other sequences. The specificity of the primer increases with the number of nucleotides that hybridize with the mutated sequence. In addition, specificity is correlated with the proportion of residues in the primer that hybridize  
35 with the mutated sequence. A primer of the present invention generally includes at least about 15 nucleotides, and usually at least about

20 nucleotides. The primer need not exceed about  
30 nucleotides, and usually does not exceed about  
25 nucleotides. In one variation of this embodiment,  
the primer includes between about 20 and about  
5 25 nucleotides. Generally, the primers should have a  $T_m$   
in the range of about 55°C to about 75°C. In practice,  
the  $T_m$  is usually between about 60°C to about 65°C to  
facilitate amplification under stringent conditions.

10

#### Vectors and Host Cells

A nucleic acid molecule of the present invention  
can be incorporated into a vector for propagation  
and/or expression in a host cell. Such vectors  
typically contain a replication sequence capable of  
15 effecting replication of the vector in a suitable host  
cell (i.e., an origin of replication) as well as  
sequences encoding a selectable marker, such as an  
antibiotic resistance gene. Upon transformation of a  
suitable host, the vector can replicate and function  
20 independently of the host genome or integrate into the  
host genome. Vector design depends, among other  
things, on the intended use and host cell for the  
vector, and the design of a heregulin variant vector  
for a particular use and host cell is within the level  
25 of skill in the art.

If the vector is intended for expression of a  
heregulin variant, the vector includes one or more  
control sequences capable of effecting and/or enhancing  
the expression of an operably linked heregulin variant  
30 coding sequence. Control sequences that are suitable  
for expression in prokaryotes, for example, include a  
promoter sequence, an operator sequence, and a ribosome  
binding site. Control sequences for expression in  
eukaryotic cells include a promoter, an enhancer, and a  
35 transcription termination sequence (i.e., a  
polyadenylation signal).

The term "operably linked" means that two nucleic acid sequences are in a functional relationship with one another. For example, a promoter (or enhancer) is operably linked to a coding sequence if it effects (or enhances) the transcription of the sequence. A ribosome binding site is operably linked to a coding sequence if it is positioned to facilitate translation. Operably linked nucleic acid sequences are often contiguous, but this is not a requirement. For example, enhancers need not be contiguous with a coding sequence to enhance transcription of the coding sequence.

A heregulin variant expression vector can also include other sequences, such as, for example, nucleic acid sequences encoding a signal sequence or an amplifiable gene. As discussed above, a signal sequence directs the secretion of a polypeptide fused thereto from a cell expressing the chimeric protein. In the expression vector, nucleic acid encoding a signal sequence is linked to a heregulin variant coding sequence so as to preserve the reading frame of the heregulin variant coding sequence. The inclusion of an amplifiable gene (e.g., the dihydrofolate reductase [DHFR] gene) in a heregulin variant expression vector allows selection of host cells containing multiple copies of the nucleic acid molecule encoding the heregulin variant.

A vector of the present invention is produced by linking desired elements by ligation at convenient restriction sites. If such sites do not exist, suitable sites can be introduced by standard mutagenesis (e.g., site-directed or cassette mutagenesis) or synthetic oligonucleotide adaptors or linkers can be used in accordance with conventional practice.

The present invention also provides a host cell containing a vector of this invention. A wide variety

of host cells are available for propagation and/or expression of vectors. Examples include prokaryotic cells (such as *E. coli* and strains of *Bacillus*, *Pseudomonas*, and other bacteria), yeast or other fungal 5 cells, insect cells, plant cells, and phage, as well as higher eukaryotic cells (such as Chinese hamster ovary cells and other mammalian cells). Host cells according to the invention include cells in culture and cells present in live animals, such as transgenic animals.

10 See U.S. Patent 5,364,934 for more information on vectors and host cells suitable for use in the recombinant production of a heregulin variant.

A vector of the present invention is introduced into a host cell by any convenient method, which will 15 vary depending on the vector-host system employed. Generally, a vector is introduced into a host cell by transformation (also known as "transfection") or infection with a virus (e.g., phage) bearing the vector. If the host cell is a prokaryotic cell (or 20 other cell having a cell wall), convenient transformation methods include the calcium treatment method described by Cohen et al., *PNAS USA* 69:2110-14 (1972), and the polyethylene glycol method of Chung et al., *Nuc. Acids. Res.* 16:3580 (1988). If a prokaryotic 25 cell is used as the host and the vector is a phagemid vector, the vector can be introduced into the host cell by infection, as described in Example 1. Yeast cells can be transformed using polyethylene glycol, for example, as taught by Hinnen, *PNAS U.S.A.* 75:1929-33 30 (1978). Mammalian cells are conveniently transformed using the calcium phosphate precipitation method described by Graham et al., *Virology* 52:546 (1978), and Gorman et al., *DNA and Protein Eng. Tech.* 2:3-10 (1990). However, other known methods for introducing 35 DNA into host cells, such as nuclear injection, electroporation (see Example 1), and protoplast fusion also are suitable for use in the invention.

In one embodiment, a host cell containing a nucleic acid molecule encoding a heregulin variant is produced by homologous recombination, as described in WO 91/06667. Briefly, this method involves

5 transforming a host cell containing an endogenous heregulin gene with a homologous recombination vector that includes the sequence to be introduced. The homologous recombination vector also includes at least one sequence of at least about 150 nucleotides in

10 length that is homologous with an endogenous sequence flanking the endogenous heregulin gene. Suitable flanking sequences are readily identified, for example, by the method of genomic walking, using a known native heregulin nucleic acid sequence as a starting point.

15 The homologous recombination vector additionally includes an amplifiable gene, such as the DHFR gene.

Transformation is carried out under conditions such that the vector integrates into the host cell genome by recombination. Cells that integrate the vector are then cultured under conditions that select for amplification of the amplifiable gene. The resulting cells are then screened for high levels of heregulin variant production.

25           Recombinant Production of Heregulin Variants

To produce a heregulin variant recombinantly, host cells containing a heregulin variant expression vector are prepared and cultured under conditions suitable for cell growth and for expression of the heregulin variant. In particular, the culture medium contains appropriate nutrients and growth factors for the host cell employed. The nutrients and growth factors required for growth of a selected host cell are, in many instances, well known or can be readily determined empirically by those skilled in the art. Suitable culture conditions for mammalian host cells, for instance, are described in Mammalian Cell Culture

(Mather ed., Plenum Press 1984), and in Barnes and Sato, Cell 22:649 (1980).

In addition, the culture conditions should allow transcription, translation, and protein transport between cellular compartments. Factors that affect these processes are well-known and include, for example, DNA/RNA copy number; factors that stabilize RNA; nutrients, supplements, and transcriptional inducers or repressors present in the culture medium; temperature, pH, and osmolality of the culture; and cell density. The adjustment of these factors to promote expression in a particular vector-host cell system is within the level of skill in the art. Principles and practical techniques for maximizing the productivity of in vitro mammalian cell cultures, for example, can be found in Mammalian Cell Biotechnology: a Practical Approach (Butler ed., IRL Press 1991).

The cell culture procedure employed in the production of a heregulin variant of the present invention can be any of a number of well-known procedures for large- or small-scale production of proteins. These include, but are not limited to, the use of a fluidized bed bioreactor, a hollow fiber bioreactor, a roller bottle culture system, and a stirred tank bioreactor system. A heregulin variant can be produced, for instance, in a batch, fed-batch, or continuous mode process.

Methods for recovery of recombinant proteins produced as described above are well-known and vary depending on the expression system employed. For example, if, as is typical, the heregulin variant is fused to a signal sequence, the heregulin variant is recovered from the culture medium or the periplasm. Conveniently, the variant is secreted into the periplasmic space as a mature protein. The heregulin variant can also be expressed intracellularly and recovered from cell lysates.

The heregulin variant can be purified from culture medium or a cell lysate by any method capable of separating the variant from components of the host cell or culture medium. Typically the heregulin variant is 5 separated from host cell and/or culture medium components that would interfere with the intended use of the heregulin variant. As a first step, the culture medium or cell lysate is usually centrifuged or filtered to remove cellular debris. The supernatant is 10 then typically concentrated or diluted to a desired volume or diafiltered into a suitable buffer to condition the preparation for further purification.

The heregulin variant is typically further purified in the same manner as the most homologous 15 native heregulin, taking account of any substantial differences in properties between the two molecules. For example, if the heregulin variant is an epitope-tagged heregulin variant, purification can be carried out using an immunoaffinity column containing antibody 20 to the epitope tag. The following exemplary procedures for purifying heregulins can be used or adapted for purifying a heregulin variant of the invention: fractionation on an immunoaffinity column, 25 fractionation on an ion-exchange column, ammonium sulphate or ethanol precipitation, reverse phase HPLC, chromatography on silica, chromatography on heparin Sepharose, chromatography on a cation exchange resin, chromatofocusing, SDS-PAGE, and gel filtration (e.g., 30 using a High Load Superdex 75<sup>TM</sup> prep grade column).

If the heregulin variant is expressed initially as 35 an insoluble, aggregated form (especially in bacterial host cells), it may be necessary to solubilize and renature the heregulin variant using techniques available in the art for solubilizing and renaturing recombinant protein refractile bodies. See, e.g., U.S. Patent No. 4,511,502.

In one variation of this embodiment, the heregulin variant is purified (1) to a degree sufficient to obtain at least 15 residues, and preferably 20 residues, of N-terminal or internal amino acid sequence, using a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue stain. As used herein, "homogeneity" means less than about 5% contamination with other source proteins, as determined by staining with Coomassie blue.

Utility of Heregulin Variants

Generally speaking, heregulin variants according to the invention can be used in the same applications as native heregulins. Of course, some heregulin variants within the scope of the invention may be better suited for one application than for other applications. However, those skilled in the art can readily ascertain which heregulin variants are appropriate for a given application by using one or more conventional assays to determine the biological activity of the variants.

*Pharmaceutical Compositions and Treatment Methods*

Heregulins are useful in treating a wide range of diseases and disorders affecting the nervous system, musculature, and epithelia. In addition, heregulins can be used in the treatment of cancer. As used herein, "treatment" encompasses the treatment of an existing disease or disorder as well as prophylactic measures.

Accordingly, the present invention provides a pharmaceutical composition including a heregulin variant that is useful in treating any of a variety of diseases or disorders. In one embodiment, a pharmaceutical heregulin variant composition is employed to treat a mammal. In particular, the

composition is useful for treating humans, farm animals (e.g., cows and sheep), zoo animals, animals used in sports (e.g., horses), and pets (e.g., dogs and cats). In a variation of this embodiment, the composition is  
5 used to treat a human patient.

A heregulin variant according to the invention can be useful in promoting the development, maintenance, and/or regeneration of a neuron in vivo. Neurons that respond to such a variant include central nervous system (brain and spinal chord) neurons, peripheral nervous system neurons (including sympathetic, parasympathetic, sensory, and enteric neurons), and motoneurons. Diseases or disorders amenable to heregulin variant treatment arise in individuals who  
10 have suffered nervous system damage due, for example, to trauma, surgery, stroke, ischemia, infection,  
15 metabolic disease, nutritional deficiency, malignancy, or a toxic agent.,

A heregulin variant can provide therapeutic benefits to such individuals by promoting the survival, proliferation, or differentiation of neurons. For example, a heregulin variant can be used to promote the survival or proliferation of motoneurons that have been damaged by trauma or surgery. A heregulin variant  
20 can also be employed to treat motoneuron disorders, such as amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and various conditions involving spinal muscular atrophy or paralysis. In addition, a heregulin variant can also be useful for  
25 treating a human neurodegenerative disorder, such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's Syndrome, nerve deafness, and Meniere's disease.

Furthermore, a heregulin variant of the invention  
30 can be used to treat neuropathy, especially peripheral neuropathy. As used herein, the term "peripheral neuropathy" refers to a disorder affecting the

peripheral nervous system, most often manifested as one or a combination of motor, sensory, sensorimotor, or autonomic neural dysfunctions. Examples include, but are not limited to, distal sensorimotor neuropathy and 5 autonomic neuropathies, such as reduced motility of the gastrointestinal tract or atony of the urinary bladder. Peripheral neuropathies amendable to heregulin variant treatment can be inherited, can result from a systemic disease, or can be induced by a toxic agent. Examples 10 of hereditary neuropathies include Charcot-Marie-Tooth disease, Refsum's disease, Abetalipoproteinemia, Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's disease, and Dejerine-Sottas syndrome. Examples of neuropathies associated with 15 systemic disease include post-polio syndrome; and examples of neuropathies induced by a toxic agent include those caused by treatment with a chemotherapeutic agent.

A heregulin variant can also be employed to 20 improve neural function. The beneficial effects of heregulin variant treatment are attributed to induction of the formation of ion channels in cell membranes and enhancement of the formation of synaptic junctions.

A heregulin variant according to the invention can 25 also be used to treat muscle cells and medical conditions affecting muscle cells. In particular, such heregulin variant can be useful for treating muscle damage, decreasing atrophy of muscle cells, and increasing muscle cell survival, proliferation and/or 30 regeneration. Examples of pathophysiological conditions of the musculature amenable to treatment with a heregulin variant include skeletal muscle diseases (e.g., myopathy or dystrophy), cardiac muscle disorders (including atrial cardiac arrhythmias, 35 cardiomyopathy, ischemic damage, congenital disease, and cardiac trauma), and smooth muscle disorders (such as arterial sclerosis, vascular lesion, or congenital

vascular disease). A heregulin variant can also be employed to reduce hypertension and to increase functional acetylcholine receptors on muscle cells (e.g., in individuals having myasthenia gravis or 5 tachycardia).

A heregulin variant of the invention can also enhance repair and/or regeneration of tissues that express ErbB receptors, especially ErbB-2 and either ErbB-3 or ErbB-4 receptors. Accordingly, a heregulin 10 variant can be useful for treating dermal wounds, gastrointestinal disease, Barrett's esophagus, cystic or non-cystic end stage kidney disease, or inflammatory bowel disease. A heregulin variant can also be employed to promote reepithelialization in the human 15 gastrointestinal, respiratory, reproductive, or urinary tract.

In addition, a heregulin variant according to the invention can be useful for inhibiting tumor cell invasion and metastasis. In particular, a tumor 20 characterized by reduced endogenous heregulin levels (Park et al., *Proc. Am. Assoc. Cancer Res.* 34:521 [1993]) is responsive to treatment with a heregulin variant of the invention. Additionally, a tumor that overexpresses ErbB receptors can be treated by using a 25 heregulin variant conjugated to a cytotoxic agent (described above) to direct the cytotoxic agent to the tumor tissue. A heregulin variant-enzyme conjugate can also be employed to target a prodrug (described above) therapy to cells expressing ErbB receptors.

30 A pharmaceutical composition according to the invention is prepared for storage by mixing a heregulin variant having the desired degree of purity with an optional physiologically acceptable carrier, excipient, or stabilizer, such as are described in Remington's 35 Pharmaceutical Sciences 16th Edition (Osol ed., 1980). The composition can be stored in the form of a lyophilized cake or an aqueous solution. A

pharmaceutically acceptable carrier, excipient, or stabilizer is non-toxic to recipients at the dosages employed, and can include a buffer (such as a phosphate buffer, citrate buffer, and buffers made from other organic acids), an antioxidant (e.g., ascorbic acid), a low-molecular weight (less than about 10 residues) polypeptide, a protein (such as serum albumin, gelatin, and an immunoglobulin), a hydrophilic polymer (such as polyvinylpyrrolidone), an amino acid (such as glycine, glutamine, asparagine, arginine, and lysine), a monosaccharide, a disaccharide, and other carbohydrates (including glucose, mannose, and dextrins), a chelating agent (e.g., ethylenediaminetetraacetic acid [EDTA]), a sugar alcohol (such as mannitol and sorbitol), a salt-forming counterion (e.g., sodium), and/or a nonionic surfactant (such as Tween™, Pluronics™, and PEG). In one embodiment, the physiologically acceptable carrier is an aqueous pH-buffered solution.

A heregulin variant composition intended for in vivo administration is typically sterile. Sterilization is readily accomplished by filtration through a sterile filtration membrane. If the composition is stored in lyophilized form, the composition can be filtered before or after 25 lyophilization and reconstitution.

A pharmaceutical heregulin variant composition of the invention is generally placed into a container having a sterile access port, such as, for example, an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle.

Methods for administering a pharmaceutical heregulin variant composition do not differ from known methods for administering therapeutic proteins. Suitable routes of administration include, for example, 35 intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial, or intralesional routes. A pharmaceutical heregulin

variant composition can be administered continuously by infusion or by bolus injection.

If desired, a sustained-release preparation can also be used to administer a heregulin variant. An exemplary sustained-release preparation has a semipermeable matrix of a solid hydrophobic polymer to which the heregulin variant is attached. Examples of suitable polymers include a polyester, a hydrogel, a polylactide, a copolymer of L-glutamic acid and 10  $\gamma$ -ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, a degradable lactic acid-glycolic acid copolymer, and poly-D-(-)-3-hydroxybutyric acid. Such matrices are in the form of shaped articles, such as films, or microcapsules.

In one embodiment, a sustained-release heregulin variant preparation includes a liposomally entrapped heregulin variant. Liposomes are small vesicles composed of various types of lipids, phospholipids, and/or surfactants. These components are typically arranged in a bilayer formation, similar to the lipid arrangement of biological membranes. Liposomes containing heregulin variants are prepared by known methods, such as, for example, those described in Epstein et al., PNAS USA 82:3688-92 (1985), and Hwang et al., PNAS USA 77:4030-34 (1980). Ordinarily the liposomes in such preparations are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the specific percentage being adjusted to provide the optimal therapy. Useful liposomes can be generated by the reverse-phase evaporation method, using a lipid composition including, for example, phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter.

For treatment of neurologic diseases or disorders, a heregulin variant can be adsorbed onto a membrane, such as a silastic membrane, which can be implanted in proximity to damaged neural tissue, as described in 5 WO 91/04014.

The dosage of a heregulin variant composition to be employed therapeutically depends, for example, upon the therapeutic objectives, the route of administration, and the condition of the patient. 10 Accordingly, it is necessary for the clinician to titer the dosage and modify the route of administration as required to obtain the optimal therapeutic effect. A typical daily dosage can range from about 1  $\mu\text{g}/\text{kg}$  to up to 100 mg/kg of body weight or more per day, but is 15 typically between about 10  $\mu\text{g}/\text{kg}/\text{day}$  to 10 mg/kg/day. Generally, the clinician begins with a low dosage of a pharmaceutical heregulin variant composition and increases the dosage until the desired therapeutic effect is achieved.

The administration of a heregulin variant of the invention can be combined with other therapeutic regimens. For the treatment of neurological conditions, a heregulin variant is optionally combined, or administered in concert, with another neurotrophic 25 factor to achieve a desired therapeutic effect. For example, a heregulin variant can be used together with nerve growth factor (NGF), a neurotrophin (e.g., NT-3, -4, or -5), bone-derived nerve factor (BDNF), an insulin-like growth factor (e.g., IGF-1 or IGF-2), 30 gas6, or another neurotrophic factor to achieve a synergistic stimulatory effect on neurons. Suitable dosages for the neurotrophic factors do not differ from those known in the art for such molecules.

For the treatment of cancer, radiation and/or a 35 chemotherapeutic agent can be administered concomitantly with a heregulin variant. Suitable preparation and dosing schedules for such

chemotherapeutic agents are as recommended by the manufacturer or as determined empirically by the clinician. For preparation and dosing schedules for standard chemotherapeutic agents, see Chemotherapy Service (Perry ed., Williams & Wilkins 1992).  
5 Administration of the chemotherapeutic agent can precede, or follow, administration of the heregulin variant, or the chemotherapeutic agent can be given simultaneously therewith. Antibodies against tumor-  
10 associated antigens, such as antibodies that bind EGFR, ErbB-2, ErbB-3, or ErbB-4 receptor, or vascular endothelial factor (VEGF) can also be co-administered with an heregulin variant, as can one or more cytokines.

15

*Non-Therapeutic Methods*

Heregulin variants according to the invention also be employed in a variety of non-therapeutic applications, such as cell culture methods and  
20 diagnostic methods. For example, a heregulin variant can be used to promote the ex vivo survival, proliferation, or differentiation of cells, such as glial, Schwann, and muscle cells. Cultures of such cells are useful for producing cell-specific factors,  
25 such as, for example, the nerve growth factor receptor ( $P75^{NGFR}$ ) which is a Schwann cell-specific factor. Cell-specific factors can be employed directly as diagnostic tools or employed to generate antibodies for diagnostic use.

30

Ex vivo cell cultures can also be used as cellular prostheses for transplantation. For example, Schwann cell cultures can be transplanted into areas of damaged spinal cord to promote regeneration of interrupted central axons or can be used to assist the repair of peripheral nerve injuries.  
35

Accordingly, the present invention provides a cell culture method in which heregulin-responsive cells are

provided in a suitable cell culture medium. Suitable tissue culture media are well known to those skilled in the art and include, but are not limited to, Minimal Essential Medium (MEM), RPMI-1640, and Dulbecco's  
5 Modified Eagle's Medium (DMEM). These tissue culture media are commercially available from Sigma Chemical Company (St. Louis, MO) and GIBCO (Grand Island, NY). The cells are cultured in the cell culture medium under conditions that permit the cells to grow in the  
10 presence of a heregulin variant. Suitable procedures for cell culture do not differ from known procedures and include, for example, liquid culture, culture in agar, and culture in a clot.

The cells are cultured in the presence of an  
15 effective amount of a heregulin variant. The amount of heregulin variant can vary, depending on the cell type and cell culture conditions, but generally is in the range of about 10, ng/ml to about 1 mg/ml. An appropriate concentration for a given cell culture can  
20 readily be determined empirically by those skilled in the art.

Techniques for culturing Schwann cells ex vivo are described in Li et al. (*supra*), and Sklar et al. (*supra*) describe ex vivo culture of clonal human  
25 myoblasts. A heregulin variant of the invention can replace the other heregulin polypeptides used in these methods.

A heregulin variant can also be employed in the diagnosis of a cancer characterized by erbB (e.g., erbB2) overexpression. In a diagnostic method  
30 according to the invention, a sample is obtained from an individual and contacted with a heregulin variant under conditions that allow specific binding between the variant and any ErbB receptors present in the  
35 sample. The sample can be a tissue sample, a bodily fluid sample, or a cell. In the case of a solid tumor, a tissue sample can be taken from a surgically removed

tumor and prepared for testing by conventional techniques. In the case of lymphomas and leukemias, a sample containing lymphocytes, leukemic cells, or lymph tissues is obtained. Other samples, including samples 5 of urine, tear drops, serum, cerebrospinal fluid, feces, sputum, cell extract, and the like, can be useful for diagnosing particular tumors. As used with regard the this method, the term "specific binding" means that the heregulin variant binds an ErbB receptor 10 with an affinity that is sufficiently high that the heregulin variant does not substantially cross-react with other components present in the sample under the suitable reaction conditions.

The amount of heregulin variant that specifically 15 binds to the sample is determined as an indication of ErbB receptor content. For example, a tissue sample can be obtained from a primary tumor and used to prepare formalin-fixed, paraffin-embedded blocks. See Muss et al., *supra*; Press et al., *Cancer Research* 20 54:2771-77 (1994). Tissue sections are then prepared according to known techniques.

A heregulin variant is contacted with a tissue section under conditions that permit specific binding between the variant and ErbB receptors present in the 25 section. Binding is generally detected using a label, such as a radioisotope, a fluorescent label, or an enzyme-substrate labelling system. The label can be conjugated directly to the heregulin variant, as described above.

30 Alternatively, the label can be bound to the heregulin variant indirectly. For example, the label can be conjugated to an anti-heregulin variant antibody or conjugated to biotin or avidin and used with an anti-heregulin variant antibody conjugated to avidin or 35 biotin (respectively), as described generally in Current Protocols in Immunology (*supra*). Selective

binding between biotin and avidin links the label to the heregulin variant.

While *in vitro* analysis is normally contemplated, *in vivo* analysis using a heregulin variant conjugated 5 to a suitable detectable label (e.g.,  $\text{In}$  for imaging) can also be performed. See, e.g., U.S. Patent No. 4,938,948.

A diagnostic method of the invention can be used in combination with other diagnostic/prognostic 10 evaluations such as determining lymph node status, primary tumor size, histologic grade, estrogen or progesterone status, tumor DNA content (ploidy), or cell proliferation (*S*-phase fraction). See Muss et al., *New Eng. J. Med.* 330:1260-66 (1994).

15 A heregulin variant according to the invention is also useful as a standard in assays for heregulins (such as a radioimmunoassay, an enzyme-linked immunoassay, and a radioreceptor assay), in an affinity purification technique (e.g., for an ErbB receptor such 20 as ErbB-3 or ErbB-4 receptor), and in a competitive receptor binding assay. A heregulin variant can also be employed as an immunogen for generating anti-heregulin variant antibodies useful in detection and/or purification of heregulin variants.

25 In addition to the applications discussed above, a heregulin variant that has an enhanced specificity for the ErbB-4 receptor, relative to the ErbB-3 receptor, can be used to bind and stimulate the ErbB-4 receptor preferentially over the ErbB-3 receptor. Such a 30 variant is useful in studies designed to distinguish between the presence of ErbB-3 and ErbB-4 receptors in a sample or to determine whether particular biological actions are mediated by one or both receptors. For instance, in cell types having a relatively small 35 number of ErbB-4 receptors and a large number of ErbB-3 receptors, in the absence of receptor-specific heregulin variants, it is difficult to identify signal

transduction pathways activated by the different receptors and to link particular biological actions to one or both receptors. A variant that preferentially binds to the ErbB-4 receptor can be used to help 5 elucidate the roles of the ErbB-3 and ErbB-4 receptors in heregulin action.

*Diagnostic Kits and Articles of Manufacture*

The present invention also provides kits useful in 10 practicing the above-described methods. In one embodiment, the invention provides a diagnostic kit, i.e., a packaged combination of reagents for use in testing a sample. The components of the kit are typically provided in predetermined ratios. A kit for 15 detecting ErbB receptors can include, for example, a heregulin variant labelled with a suitable label or a heregulin variant with a labelled reagent(s) for indirect labelling. If the label is an enzyme, the kit typically includes any substrate or cofactor required. 20 by the enzyme label. Other additives, such as stabilizers, buffers and the like, can also be included in the kit. Kit reagents can be provided as dry powders, usually lyophilized, together with excipients for preparing kit reagent solutions of the appropriate 25 concentration. Kits also typically include instructions for carrying out the assay for which the kit is designed.

The present invention also provides an article of manufacture containing a pharmaceutical heregulin 30 variant composition useful for the treatment of a disorder described above. The article of manufacture includes a container and a label. Suitable containers include, for example, bottles, vials, syringes, and test tubes. The container can be made from any of 35 a variety of materials, such as glass or plastic and can have a sterile access port. The label on, or

associated with, the container indicates the disorder that the composition is to be used to treat.

The article of manufacture can be a component of a kit that includes a second container including a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution, or dextrose solution. The kit can also include other materials that are desirable from a commercial or user standpoint, such as other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

The following examples are offered by way of illustration and not by way of limitation. The disclosures of all citations in the specification are expressly incorporated herein by reference.

#### EXAMPLE 1

##### *Determination of the Heregulin- $\beta$ 1*

##### *Minimal EGF-Like Domain*

The smallest portion of HRG- $\beta$ 1 EGF that provides high-affinity receptor binding in the context of phage display was determined by preparing phagemid vectors that produced HRG- $\beta$ 1 147-227, 147-244, 177-227, or 177-244 fused to the C-terminus of M13 pIII. These HRG- $\beta$ 1 EGF-like domain fragments were amplified from the vector pHL89 (which is described in Holmes, et al., *Science* 256: 1205-10 [1992]) by PCR with primers having NsiI/XbaI-containing overhangs.

These fragments were inserted into the phagemid display vector pam-g3 by restriction digest-ligation at the same sites to generate constructs pHRG1-g3 (177-227), pHRG2-g3 (177-244), pHRG4-g3 (147-227), and pHRG5-g3 (147-244). pam-g3 was a derivative of phGHam-g3, which was designed for phage display of human growth hormone (hGH) and was described in Lowman et al., *Biochemistry* 30:10832-38 (1991). pam-g3 was produced by removing the hGH gene present in phGHam-g3

and replacing this gene with a stuffer fragment, which provides space for cleavage at the restriction sites used for cloning.

pHRG1-g3 contained an Ala227Val mutation that had  
5 been introduced in generating the construct. Single-stranded uracil-containing template was produced from this construct and used in site-directed mutagenesis to restore Ala227, generating pHRG6-g3 (177-227). In each of the above-described constructs, the HRG- $\beta$ 1 EGF-like  
10 domain fragment was attached to residue 247 of pIII.

In an effort to determine whether the inclusion of an extended flexible linker at the junction between HRG- $\beta$ 1 EGF and pIII would alleviate potential pIII interference of binding to ErbB-3, two constructs  
15 having linkers at this junction were prepared from the pHRG1-g3 template. pHRG8-g3 expressed HRG- $\beta$ 1 177-228 attached to pIII 323 through a linker containing three consecutive GGGS (SEQ ID NO:34) repeats, and pHRG11-g3 expressed HRG- $\beta$ 1 177-230 attached to pIII 247 through a  
20 GGGSGGG (SEQ ID NO:35) linkage.

The HRG- $\beta$ 1 EGF-like domains expressed from the above-described constructs are designated herein by removing the "p" and the "-g3" that appear in the name of the construct. Thus, the HRG- $\beta$ 1 EGF-like domain expressed from the pHRG2-g3 construct is designated "HRG2."

The domains were displayed monovalently on phage as pIII fusion proteins, as described by Bass et al., *Proteins* 8:309-14 (1990), and then analyzed for their  
30 binding to the high-affinity ErbB-2/3 receptor-Ig fusion (ErbB-2/3-Ig) using the phage ELISA technique described by Cunningham et al., *EMBO J.* 13:2508-15 (1994), with slight modifications. To produce phage displaying the domains, mutagenesis reaction mixtures  
35 were electrotransformed into XL1-Blue<sup>TM</sup> cells (Stratagene, Inc., La Jolla, CA), according to the manufacturer's protocol. The transformed cells were

then infected with  $10^{11}$  plaque-forming units (pfu) M13K07 helper phage (Promega Corp., Madison, WI). Phage stocks (about  $10^{14}$  phagemid/mL) were prepared by precipitating culture broths from the cells after 5 18-24 hours (h) of growth with 20% PEG(2000)/2.5 M NaCl, according to the method of Sambrook and Maniatis, Molecular Cloning a Laboratory Manual Cold Spring Harbor Press 429 (1989). The phage were resuspended in phosphate-buffered saline (PBS: 0.01 M sodium 10 phosphate, 0.1 M NaCl, pH 7.5).

ErbB receptor-Ig fusions were prepared using vectors that expressed the extracellular domain (ECD) of the ErbB-2, ErbB-3, or ErbB-4 receptor fused to a human IgG constant domain. First, a unique MluI site 15 was engineered into a vector expressing a human IgG heavy chain (pDR2) at the region encoding the hinge domain of the immunoglobulin. MluI sites were also engineered into a set of ErbB expression vectors at the region encoding the ECD/transmembrane junctions of 20 these receptors. All mutagenesis was performed according to the method of Kunkel et al., *Methods Enzymol.* 154:367-82 (1987).

The MluI sites were used to make constructs that expressed the desired ErbB receptor-Ig fusion. The 25 fusion junctions of the various receptor fusions were as follows (in order from the N-terminus to the C-terminus): for ErbB-2, Glu646 of ErbB2 was fused to Thr-Arg-Asp-Lys-Thr (TRDKT; SEQ ID NO:36), which was fused to His224 of VH ( $H224_{VH}$ ); for ErbB-3, Leu617 of 30 ErbB-3 was fused to TRDKT- $H224_{VH}$ ; for ErbB-4, Gly640 of ErbB-4 was fused to TRDKT- $H224_{VH}$ . The ErbB receptor residue numbers are indicated according to the numbering system of Plowman et al. *PNAS USA* 90:1746-50 35 (1993). The conserved TR sequence was derived from the MluI site, and the conserved DKT sequence was derived from a linker. The final expression constructs had a

pRK-type plasmid backbone wherein eukaryotic expression was driven by a cytomegalovirus (CMV) promoter.

Receptor fusions were expressed from these constructs, purified, and allowed to form disulfide-linked dimers. Homodimeric ErbB-2, ErbB-3 and ErbB-4 receptor-Ig fusions were produced by transfecting cells with the construct encoding the appropriate receptor fusion. Heterodimeric receptor fusions were generated by co-transfected two expression vectors encoding different receptor fusions into the same cells. The resulting secreted receptor fusions were mixtures of two types of homodimers and the expected heterodimer.

To express the receptor fusions, adherent HEK-293 cells (ATCC No. CRL1573) were transfected with the appropriate expression vector(s) using the calcium phosphate precipitation method described by Gorman et al., *DNA and Protein Eng. Tech.* 2:3-10 (1990). Serum-containing medium was replaced with serum-free medium at 15 h post-transfection, and the transfected cells were cultured serum-free for 5-7 days.

The resulting conditioned medium was harvested and passed through Protein A columns (1 mL Pharmacia HiTrap™, Piscataway, NJ). Purified receptor fusions were eluted with 0.1 M citric acid (pH 4.2) into tubes containing 1 M Tris-HCl (pH 9.0). The eluted proteins were then dialyzed against PBS and concentrated using Centri-prep-30™ filters (Amicon, Beverly, MA). Glycerol was added to a final concentration of 25%, and the preparations stored at -20°C. The receptor fusion concentration was determined via a Fc-ELISA.

Microtiter plates (Nunc Maxisorp™ 96-well plates, Inter Med, Denmark) for phage ELISA were prepared as follows. The wells were precoated overnight with 0.5 µg of rabbit anti-human IgG (Fc gamma fragment-specific) antibodies (Jackson Immunoresearch, West Grove, PA) in 100 µL 50 mM NaCO<sub>3</sub> (pH 9.6). The wells were blocked for 30 minutes (min) with 200 µL PBS

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containing 0.1% bovine serum albumin (BSA) and rinsed with wash buffer (PBS containing 0.05% Tween 20<sup>TM</sup>). The wells were then coated with 0.1 µg ErbB-2/3-Ig in binding buffer (PBS, 0.1% BSA, 0.05% Tween 20<sup>TM</sup>) for 5 h, and washed again.

Serial dilutions of soluble ErbB-2/3-Ig (competitor) and a concentration of phage predetermined to give 60% saturation (without competitor) were added to the wells in 100 µL binding buffer. Following 10 incubation for 2 h at room temperature, plates were washed extensively and treated with a 1:900 dilution of anti-M13 horseradish peroxidase conjugate (Pharmacia, Piscataway, NJ) for 20 min. The amount of phage binding was determined by assaying horseradish 15 peroxidase activity using o-phenylenediamine dihydrochloride substrate solution (Sigma Chemical Company, St. Louis, MO). EC<sub>50</sub> values were calculated as the concentration of soluble ErbB-2/3-Ig required to compete half of the phage off the plate.

20 The results are set forth in Table 3.

Table 3  
Initial Heregulin-Phage Variants

25	Construct	Heregulin-β1 residues	Linker and pIII fusion point	ErbB-2/3-Ig EC <sub>50</sub> (nM)
	HRG2	177-244	pIII 247	6.0
	HRG4	147-227	pIII 247	38.0
	HRG5	147-244	pIII 247	4.7
	HRG6	177-227	pIII 247	40.0
30	HRG7	177-228	pIII 247	42.0
	HRG8	177-228 (1-52)	(GGGG),-pIII 323	11.0
	HRG11	177-230	GGGSGGG-pIII 247	19.0

'Average of duplicate experiments

35 All phage stocks bound specifically to immobilized ErbB-2/3-Ig and could be competed off with similar EC<sub>50</sub> values (5-42 nM). These values were about 100-fold higher than the previously measured dissociation

constant ( $K_d$ ). Holmes, et al., *supra*. However, EC<sub>50</sub> values obtained from phage ELISA are often higher than the true  $K_d$ , particularly for high-affinity interactions. This may be due to the high receptor 5 coat concentration required to give a reasonable signal for the bound phage, a low percentage of active receptor in competitor solutions, or interference from the linkage of the protein to pIII.

In any event, the HRG- $\beta$ 1 147-176 did not appear to 10 enhance the binding of phage displaying the HRG- $\beta$ 1 EGF-like domain to ErbB-3-Ig, whereas HRG- $\beta$ 1 228-244 contributed slightly to binding affinity. Thus, the minimal EGF-like domain of HRG- $\beta$ 1 was defined as HRG- $\beta$ 1 177-228.

15 Phage ELISA was also carried out for the constructs encoding HRG- $\beta$ 1 EGF-pIII fusions containing linkers inserted between HRG- $\beta$ 1 EGF and the pIII fragment. Mild enhancements in binding affinity were observed for the linker-containing fusions, along with 20 increased expression of functional fusions, as determined by binding titrations of the phage stocks. The fusion of HRG- $\beta$ 1 EGF via a linker to pIII residue 323, instead of residue 247 (pHRG8-g3) resulted in a slight affinity enhancement. 25 This construct was therefore used as the template vector for construction of phage display libraries.

#### EXAMPLE 2

##### Identification of Active Residues in the Heregulin- $\beta$ 1 EGF Domain by Alanine Scanning

30 This example describes the identification of active residues in the heregulin- $\beta$ 1 (HRG- $\beta$ 1) EGF-like domain (HRG- $\beta$ 1 177-229) that play a role in the binding of HRG- $\beta$ 1 to the ErbB-3 and ErbB-4 receptors. Active 35 residues were identified by mutating individual amino acids in this domain to alanine. The mutated domains (hereinafter "variants") were displayed monovalently on

phage as pIII fusion proteins and variant affinities for ErbB-3 and ErbB-4 were determined by phage ELISA. Selected variants were expressed as thioredoxin fusion proteins, which were also assayed for ErbB-3 and ErbB-4 affinity.

#### *Alanine Scanning Mutagenesis and Phage Display*

Alanine-substituted variants were generated by site-directed mutagenesis according to Kunkel et al., 10 *Methods Enzymol.* 154:367-82 (1987) (hereinafter "Kunkel mutagenesis"), using uracil-containing single-stranded DNA template prepared from pHRG2-g3. pHRG2-g3, which is described in Example 1, expressed HRG- $\beta$ 1 177-244 fused to pIII 247. A series of oligonucleotides was 15 used to generate a series of constructs that expressed a series of variants in which consecutive residues were mutated to alanine. Phage stocks were prepared from these constructs as described in Example 1, except that PEG(8000) was used to precipitate the phage. The 20 affinities of the alanine-substituted variants for ErbB-3-Ig and ErbB-4-Ig was determined by phage ELISA as described in Example 1. The results are shown in Figure 2, which indicates the ratio of the EC<sub>50</sub> for each 25 variant compared to the EC<sub>50</sub> for wild-type HRG- $\beta$ 1 177-224, also displayed on phage. In this plot, a ratio of one indicates that there was no difference in affinity for variant binding compared to wild-type HRG- $\beta$ 1 177-224, and a ratio of, e.g., five indicates that the 30 variant bound the receptor with an affinity five-fold less than that of wild-type HRG- $\beta$ 1 177-224.

#### *Expression, Purification, and Assay of Soluble Alanine-Substituted Variants*

A number of alanine-substituted variants were 35 expressed in soluble form as thioredoxin (Trx) fusion proteins. To prepare suitable expression vectors, a Trx expression vector was first generated from pET23a

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(Novagen, Inc., Madison, WI). pET23a was digested with NdeI (which cuts at base 238) and HindIII (which cuts at base 173), and a fragment encoding Trx was inserted. This fragment was obtained from pTrxFus (bases 2722-  
5 3180; Invitrogen Corp., San Diego, CA). The NdeI site, which includes the Trx translation start site, was then destroyed by cutting with NdeI and religating with Klenow. This removed the NdeI site, while retaining the Trx translation start.

10 Vectors encoding HRG- $\beta$ 1 alanine-substituted variants were initially generated by Kunkel mutagenesis in a pRK5.gDhrgB1 vector (described in Gorman et al., DNA Prot. Eng. Tech. 2:2-10 [1990]). The sequences encoding the variants could be cleaved from these  
15 vectors using NdeI and BamHI. To facilitate cloning of such fragments into the Trx expression vector, Kunkel mutagenesis was used to engineer a KpnI site into the pRK5.gDhrgB1 vector encoding wild-type HRG- $\beta$ 1 146-244 immediately upstream of the NdeI site (at base 5407).  
20 A KpnI-BamHI fragment encoding wild-type HRG- $\beta$ 1 146-224 was then cleaved from pRK5.gDhrgB1 and inserted to the Trx expression vector at KpnI and BamHI cloning sites at the 3' end of the sequence encoding Trx. This introduced an NdeI site immediately downstream of the  
25 KpnI site. In the resultant vector, the wild-type HRG- $\beta$ 1 sequence could be removed by digesting with NdeI and BamHI and replaced with an NdeI-BamHI fragment encoding a variant. The series of Trx-variant expression vectors thus obtained expressed Trx-variant fusions that contained an enterokinase protease  
30 recognition site (DDDDK; SEQ ID NO:37) between the Trx and the variant sequences.

Expression of Trx-variant fusion proteins was driven by the inducible T7 promoter from pET23a.  
35 Cloning, cell growth, and expression were carried out as described in the Novagen pET system manual. Briefly, cloning was done in XL1-Blue™ cells

(Stratagene, Inc., La Jolla, CA) and expression of soluble protein in BL21DE3 host cells (Novagen, Inc., Madison, WI). BL21DE3 cells containing a Trx-variant expression vector were grown at 37°C in LB medium until 5 the OD<sub>550</sub> reached 0.3-0.6. Expression of Trx-variant was then induced by addition of 0.4 nM isopropyl-β-D-thiogalactopyranoside (IPTG), and growth was allowed to continue for 2-4 h at 28°C. Cells were collected by centrifugation, resuspended in 0.02 M Tris-HCl, 0.025 M 10 EDTA (pH 7.5) to a volume that was 1/20th the cell culture volume.

Cells were lysed by freezing on dry ice, thawing at 37°C, followed by vigorous sonication. The freeze, thaw, and sonication cycle was repeated three times.

15 Protein was further solubilized in 6 M GdHCl, 0.1 M Tris-HCl (pH 8.8), sulfitolized by the addition of 0.1 M Na<sub>2</sub>SO<sub>3</sub>, 0.2 M Na<sub>2</sub>S<sub>4</sub>O<sub>6</sub>, and stirred at room temperature for 1.5 h. Protein was dialyzed into 0.05 M Tris-HCl (pH 7.5), 0.01 M methionine. After 20 dialysis, the insoluble material was removed by centrifugation at 35K x g for 15 min.

The supernatant was purified by Fast Flow Q Sepharose™ (Pharmacia, Piscataway, NJ) chromatography using a 15-ml column equilibrated with 0.01 M Tris-HCl (pH 7.5). Protein was eluted using a 0-2 M NaCl gradient with a flow rate of 5 mL/min. The Trx-variant fusions eluted between 0.5-0.6 M NaCl and were refolded overnight at room temperature after addition of 1 mM cysteine. The resultant preparation was dialyzed into 30 0.05 M Tris-HCl (pH 7.5), 0.01 M methionine. Trx-variant fusions were found to be essentially homogeneous as determined by amino acid analysis and SDS-PAGE.

35 The affinities of the Trx-variant fusions for ErbB receptor-Ig fusions were determined by measuring inhibition of <sup>125</sup>I-HRG-β1 177-244 binding to ErbB-3-Ig and ErbB-4-Ig. Receptor fusions were coated on plates

(Nunc Maxisorp C™ break-apart strip wells, Inter Med, Denmark) via anti-human IgG, as described in Example 1 for phage ELISA. Binding assays were carried out with a constant amount of  $^{125}\text{I}$ -HRG- $\beta$ 1 177-244 (100-300 pM) and varying concentrations (100 pM - 4  $\mu\text{M}$ ) of unlabeled Trx-variant fusion. Following incubation for 1-3 h at room temperature, plates were washed, and the amount of bound  $^{125}\text{I}$ -HRG- $\beta$ 1 177-244 in each well was counted on a gamma counter (Isodata, ICN Biomedic Systems, Huntsville, AL). For the ErbB-3 binding assays, the blocking buffer was TBST (0.025 M Tris-HCl [pH 7.5], 0.15 M NaCl, 0.02% Tween 20™) containing 1% BSA; the binding buffer was RPMI 1640™ cell culture media (Gibco-BRL, Gaithersburg, MD) containing 2 mM glutamine, 100 U/mL penicillin, 100  $\mu\text{g}/\text{mL}$  streptomycin, 10 mM HEPES buffer (pH 7.2), 0.2% BSA; and the wash buffer was TBST. For the ErbB-4 binding assays, PBS containing 1% BSA, was used as the blocking and binding buffers, and the wash buffer was PBS containing 0.05% Tween 20™.

The results are shown in Tables 4 and 5.

Table 4

*EC<sub>50</sub>* Values for Phage and Soluble Alanine-Substituted  
Variant Binding to the ErbB-3 Receptor

5

	<u>Variant*</u>	<u>Phage EC<sub>50</sub> (nM)</u>	<u>Sol EC<sub>50</sub> (nM)</u>
	HRG-β1*	13	9
	TH-WT*		47.6
10	S177	67	129
	H178	>1000	476
	L179	~1000	394
	F189	892	975
	N192	>1000	1642
15	G193	>1000	26.9
	G194	500	1212
	E195	>1000	42
	V199	27	
	K200	20	45.4
20	P205	22	39.5
	R207	>1000	245
	K211	>1000	248
	E215	51	156
	F216	500	2550
25	T217	>1000	145
	G218	>1000	668
	R220	>1000	no binding
	Y224	865	339
	F229	6	177

30

\*Variants are identified by the HRG-β1 residues mutated to alanine.

35

\*HRG-B1 is recombinantly produced HRG-β1 177-244.

\*TH-WT is thioredoxin fused at its C-terminus to wild-type HRG-β1 146-244.

Table 5

*EC<sub>50</sub>* Values for Phage and Soluble Alanine-Substituted Variant Binding to the ErbB-4 Receptor

5

	<u>Variant*</u>	<u>Phage EC<sub>50</sub> (nM)</u>	<u>Sol EC<sub>50</sub> (nM)</u>
	HRG- $\beta$ 1*	19	14.8
	TH-WT <sup>a</sup>		15.4
10	S177	83	54.6
	H178	32	138
	L179	56	51.7
	F189	106	565
	N192	188	696
15	G193	23	76.3
	G194	65	275
	E195	24	13.2
	V199	47	246
	K200	25	16.9
20	P205	8	34.2
	R207	30	24.3
	K211	59	124
	E215	32	104
	F216	>1000	173
25	T217	14.2	32.7
	G218	>1000	608
	R220	>1000	no binding
	Y224	51	24.5
	F229	>1000	89.9

30

\*Variants are identified by the HRG- $\beta$ 1 residues mutated to alanine.

35

\*HRG-B1 is recombinantly produced HRG- $\beta$ 1 177-244.

<sup>a</sup>TH-WT is thioredoxin fused at its C-terminus to wild-type HRG- $\beta$ 1 146-244.

## EXAMPLE 3

Selection of Heregulin- $\beta$ 1 EGF Domain Variants  
Using Monovalent Phage Display

5 This example describes the selection HRG- $\beta$ 1 variants containing residues corresponding to the minimal EGF-like domain (HRG- $\beta$ 1 177-228). For these variants, residue numbers also are expressed, in parentheses, in terms of the position of the residue in 10 the minimal EGF-like domain (i.e., HRG- $\beta$ 1 EGF 1-52).

Variants of HRG- $\beta$ 1 EGF were prepared and selected 15 for binding to ErbB-3-Ig using monovalent phage display, according to the method of Bass et al., *Proteins* 8:309-14 (1990). As discussed in detail below, an HRG- $\beta$ 1 EGF phagemid vector was prepared, in which HRG- $\beta$ 1 EGF was fused to a C-terminal fragment of the M13 coat protein pIII. Kunkel mutagenesis was performed to introduce stop codons into this vector at sites selected for randomization. This step ensures 20 that the starting vector is incapable of expressing the wild-type polypeptide. Stretches of four to six residues per library were randomized in a linear fashion, except for the six cysteines, Phe189 (HRG- $\beta$ 1 EGF Phe13) and the two most C-terminal residues (see 25 Figure 3). Phe189 was not altered because this residue is conserved as an aromatic residue in EGF and TGF- $\alpha$  and forms a stacking interaction with Tyr208 (HRG- $\beta$ 1 EGF Tyr32) Jacobsen et al., *Biochemistry* 35:3402-17 (1996). HRG- $\beta$ 1 EGF was thus covered in 30 eight libraries, designated A-E, G, H and I.

Library E, covering HRG- $\beta$ 1 202-209 (HRG- $\beta$ 1 EGF 26-33), contained a three-residue deletion. The deleted region corresponds to a disordered turn between the second and third  $\beta$ -sheet of HRG- $\beta$ 1 EGF, and the 35 equivalent amino acids are absent in EGF and TGF- $\alpha$ . An HRG- $\beta$ 1 EGF control variant in which HRG- $\beta$ 1 202-204 (HRG- $\beta$ 1 EGF 26-28) of HRG8 are deleted (HRG63) bound

ErbB-3-Ig with an affinity similar to that of wild-type (Table 13).

An additional library (F) was created to randomize a surface patch composed of side chains from the first 5 and second  $\beta$ -sheets, which included HRG- $\beta$ 1 178, 180, 198, and 200 (HRG- $\beta$ 1 EGF 2, 4, 22, and 24).

The selected sites in the starting vectors were randomized by Kunkel mutagenesis to produce HRG- $\beta$ 1 EGF libraries. Phage displaying mutated HRG- $\beta$ 1 EGFs were produced from the libraries under conditions such that, statistically, each phage particle displayed no more than one copy of the mutated HRG- $\beta$ 1 EGF. See 10 Bass et al., *supra*. These phage were then selected for binding to (sorted against) ErbB-3-Ig immobilized on an 15 ELISA plate. Bound phage were eluted and used to reinfect host cells, which were used to produce new phage for another round of sorting. This process was repeated six to seven times for each library. Twelve 20 clones from the phage selected from each library were then sequenced.

#### *Construction of Phage Libraries*

Phage libraries were constructed by Kunkel mutagenesis using uracil-containing single-stranded DNA template prepared from pHRG8-g3. pHRG8-g3, which is 25 described in Example 1, expressed HRG- $\beta$ 1 177-228 (HRG- $\beta$ 1 EGF 1-52) fused via a linker to pIII residue 323. For each library, TAA and TGA stop codons 30 were installed at positions selected for randomization to generate custom templates that eliminated wild-type background from the pools. Positions were fully randomized by mutation to NNS codons (where N is any of the four bases and S is either G or C). One oligonucleotide was used for each library mutagenesis 35 reaction except for Library F, for which two oligonucleotides (one randomizing HRG- $\beta$ 1 178 and 180 [HRG- $\beta$ 1 EGF 2 and 4] and the other randomizing HRG- $\beta$ 1

198 and 200 [HRG- $\beta$ 1 EGF 22 and 24]), were used simultaneously. Mutagenesis oligonucleotides contained 18-base overhangs on either side of the randomized residues.

5       Mutagenesis reaction mixtures were electro-transformed into XL-1 blue cells (Stratagene, Inc., La Jolla, CA), according to the manufacturer's protocol. The transformed cells were then infected with  $10^{11}$  pfu M13K07 helper phage (Promega Corp., 10 Madison, WI), and phage stocks (about  $10^{14}$  phagemid/mL) were prepared as described in Example 1.

Between  $1.0 \times 10^8$  and  $6.4 \times 10^8$  transformants were obtained for each library, meaning that the libraries containing five or fewer randomized codons had 15 excellent representation of the possible amino acid sequence combinations ( $3.36 \times 10^7$  possible DNA sequences;  $3.2 \times 10^6$  possible amino acid sequences). Library B, containing six randomized codons ( $1.1 \times 10^9$  DNA sequences), had  $4.8 \times 10^8$  total transformants.

20

#### *Selection of Phage for ErbB-3-Ig Binding*

Monovalent phage were prepared and the selection performed on ErbB-3-Ig prebound to microtiter plates via capture with polyclonal antibodies to the human Fc fragment, as described in Example 1. Approximately  $10^{12}$  phage in  $100 \mu\text{L}$  binding buffer (PBS, 0.1% BSA, 0.05% Tween 20<sup>TM</sup>) were applied to an ErbB-3-Ig-coated well and a control well to which no ErbB-3-Ig had been added. Following a 2 h incubation at room temperature, the 30 plates were washed extensively (12x) and phage eluted by adding  $100 \mu\text{L}$  of a solution of 50 mM HCl and 0.05% Tween<sup>TM</sup> 20 and shaking for 10 min.

Eluates were neutralized with  $10 \mu\text{L}$  1 M Tris-HCl (pH 8.0) and  $20 \mu\text{L}$  used for titration on log-phase XL-1 35 blue cells. The remainder was used to infect 1 mL of log-phase XL-1 blue cells (30 min at 37°C), which were then superinfected with  $2 \times 10^{10}$  pfu M13K07 phage and

grown in 25 mL 2YT broth (16 g/L tryptone, 10 g/L yeast extract, 5 g/L NaCl) containing 50 µg/mL carbenicillin for 18-24 h. Phage were harvested as described above and the cycle repeated. The libraries enriched  
5 rapidly, such that by round six of selection the ratio of phage eluted from positive (ErbB-3-Ig-coated) wells to negative (anti-hu Fc precoat only) wells was between 39 and 9200.

After round six (libraries A, B, D-F) or round  
10 seven (libraries C, G-I) of selection, twelve clones from each library were randomly picked and sequenced by the dideoxy method. See Sanger et al., PNAS USA 74:5463-67 (1977). The amino acids at the randomized positions deduced from the DNA sequences are shown in  
15 Tables 6-12 (a " ." indicates a residue that is identical to the wild-type residue). The consensus selected residues at each position are displayed graphically in Figure 3. In general, there were a large number of mutations, in some cases with dramatic  
20 changes in the character of the side chains. At several positions that sorted to a particular residue, a mixture of DNA codons was found, providing confidence that the libraries had large diversity and that  
25 selection was at the protein level. In several of the libraries, there was a spontaneous mutation of HRG- $\beta$ 1 Met226Ile (HRG- $\beta$ 1 EGF Met50Ile) due to a one-base change in this codon. This mutation results in a significant affinity enhancement for ErbB-3-Ig binding.  
The sequencing results for each library are summarized  
30 below.

Library A - HRG- $\beta$ 1 177-181 (HRG- $\beta$ 1 EGF 1-5)

HRG- $\beta$ 1 177-181 (HRG- $\beta$ 1 EGF 1-5) is present in the first  $\beta$ -strand in the wild-type N-terminal subdomain.  
35 The amino acid changes in the variants selected from this library are shown in Table 6.

Table 6  
Library A Variants

Variant No.	Position in HRG- $\beta$ 1				
	177	178	179	180	181
5 Wild-type	S	H	L	V	K (SEQ ID NO:38)
1	W	R	.	.	P (SEQ ID NO:39)
2	W	S	.	Q	P (SEQ ID NO:40)
3, 5, 10	W	E	.	.	P (SEQ ID NO:41)
4	W	S	.	.	(SEQ ID NO:42)
10 6	W	S	.	I	P (SEQ ID NO:43)
7	W	R	.	.	A (SEQ ID NO:44)
8	W	A	.	.	P (SEQ ID NO:45)
9	W	S	.	Q	.
11	W	E	.	.	A (SEQ ID NO:47)
15 12	W	S	.	E	P (SEQ ID NO:48)

Upon randomization, Ser177 (Ser1) sorted exclusively to Trp. His178 (His2) sorted to mixed hydrophilic residues, but the wild-type residue was not among them. Leu179 (Leu3) was conserved in all variants sequenced. Val180 (Val4) sorted to wild-type in eight out of 12 variants, and the remaining variants had conservative substitutions at this position, with the exception of a Val180Glu (Val4Glu) mutation. At Lys181 (Lys5), Pro appeared in eight variants, and the wild-type residue was found in two variants.

Four variants from library A did not contain amino acid substitutions at positions randomized in library A. Instead, these variants contained amino acid substitutions at positions randomized in library B, and thus these variants are listed as variants B1-B4 in Table 7. Similarly, four variants from library B did not contain amino acid substitutions at positions randomized in library B, but rather contained substitutions at positions randomized in

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library A. These variants are listed as variants A5-A8 in Table 6.

5      *Library B - HRG- $\beta$ 1 183-188 (HRG- $\beta$ 1 EGF 7-12)*

HRG- $\beta$ 1 183-188 (HRG- $\beta$ 1 EGF 7-12) has a helical character in the wild-type protein. The amino acid changes in the variants selected from this library are shown in Table 7.

10

Table 7  
*Library B Variants*

15	Variant No.	Position in HRG- $\beta$ 1						(SEQ ID NO:49)
		183	184	185	186	187	188	
	Wild-type	A	E	K	E	K	T	
	1*	G	V	G	R	D	G	(SEQ ID NO:50)
	2*	G	G	E	R	E	G	(SEQ ID NO:51)
20	3	G	.	E	R	E	G	(SEQ ID NO:52)
	4*, 5*	G	W	D	R	E	G	(SEQ ID NO:53)
	6*	G	V	Q	R	E	G	(SEQ ID NO:54)
	7	G	.	E	R	A	G	(SEQ ID NO:55)
	8	G	K	E	R	E	G	(SEQ ID NO:56)
25	9*	T	N	S	R	E	G	(SEQ ID NO:57)
	10*	D	K	S	R	E	G	(SEQ ID NO:58)
	11*	G	.	D	R	.	Q	(SEQ ID NO:59)
	12	G	R	E	R	E	G	(SEQ ID NO:60)

30      \*Variant also contained Met226Ile.

Randomization of this region produced the most dramatic changes from the wild-type sequence, although the generally hydrophilic character of this region was maintained in the variants sequenced. In particular, this six-residue stretch sorted to Gly residues at the first and last positions, Ala183 and Thr188 (Ala7 and Thr12). There was also a change in registry of

positive and negative charges at Lys185 (Lys9), which sorted to Glu and Asp, among others; Glu186 (Glu10), which sorted exclusively to Arg; and Lys187 (Lys11), which sorted to Glu and Asp. Glu184 (Glu8) sorted to a variety of different types of residues, indicating that this side chain does not play an important role in ErbB-3 receptor binding.

Library C - HRG- $\beta$ 1 191-195 (HRG- $\beta$ 1 EGF 15-19)

10 HRG- $\beta$ 1 191-195 (HRG- $\beta$ 1 EGF 15-19) includes the  
 $\beta$ -turn between the helix and the second  $\beta$ -strand. The  
amino acid changes in the variants selected from this  
library are shown in Table 8.

15 Table 8  
*Library C Variants*

		Position in HRG- $\beta$ 1					
		191	192	193	194	195	
Variant No.		V	N	G	G	E	(SEQ ID NO:61)
20	Wild-type	.	.	.	.	.	(SEQ ID NO:62)
	1, 2, 4, 5, 7-12	.	.	.	.	V	(SEQ ID NO:63)
	3	.	.	.	.	Q	(SEQ ID NO:64)
	6	.	.	.	.		

Randomization and selection produced variants in which the wild-type amino acid sequence in this region was almost completely conserved. Mutations were found in only two variants, both at Glu195 (Glu19). This result is consistent with an important role for the wild-type residues in this region in ErbB-3 receptor binding.

*Library D - HRG- $\beta$ 1 197-201 (HRG- $\beta$ 1 EGF 21-25)*

HRG- $\beta$ 1 197-201 (HRG- $\beta$ 1 EGF 21-25) is present in the second  $\beta$ -strand in the N-terminal subdomain. The amino acid changes in the variants selected from this 5 library are shown in Table 9.

Table 9  
*Library D Variants*

10 Position in HRG- $\beta$ 1

Variant No.	197	198	199	200	201	(SEQ ID NO:65)
Wild-type	F	M	V	K	D	
1*, 2*, 8*, 12*	Y	K	.	R	I	(SEQ ID NO:66)
15 3	.	R	.	.	T	(SEQ ID NO:67)
4, 5, 7, 9	Y	R	.	.	T	(SEQ ID NO:68)
6	Y	.	I	.	Y	(SEQ ID NO:69)
10	Y	.	.	.	T	(SEQ ID NO:70)
20 11	M	R	.	R	T	(SEQ ID NO:71)

\*Variant also contained Met226Ile.

Randomization in this region yielded either a gain or loss of charge for two of the five residues. Phe197 (Phe21) sorted to Tyr in 10 out of 12 variants, 25 maintaining aromaticity at this position. Met198 (Met22) sorted to a positively charged residue in 11 out of 12 variants. Val199 (Val23) was conserved in all variants, and Lys200 (Lys24) sorted either to wild-type or to Arg, retaining the positive charge at 30 this position. Asp201 (Asp25) sorted to uncharged residues Thr or Ile, retaining the  $\beta$ -branch character of this position. Variants D1, D2, D8, D12 also 35 included the spontaneous affinity-enhancing Met226Ile (Met50Ile) mutation.

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Library E - HRG- $\beta$ 1 205-209 (HRG- $\beta$ 1 EGF 29-33)  
HRG- $\beta$ 1 205-209 (HRG- $\beta$ 1 EGF 29-33) includes  
residues present in the third  $\beta$ -strand in the  
N-terminal subdomain. The amino acid changes in the  
5 variants selected from this library are shown in  
Table 10.

Table 10  
Library E Variants

10

Position in HRG- $\beta$ 1

Variant No.	205	206	207	208	209	(SEQ ID NO:72)
Wild-type	P	S	R	Y	L	
15      1	T	P	Y	L	M	(SEQ ID NO:73)
2, 4	Y	G	Y	L	M	(SEQ ID NO:74)
3*	Y	R	Y	R	M	(SEQ ID NO:75)
5, 12	T	H	Y	R	G	(SEQ ID NO:76)
6	T	H	Y	R	M	(SEQ ID NO:77)
20      7*	Y	K	Y	R	M	(SEQ ID NO:78)
8, 9	T	K	Y	R	G	(SEQ ID NO:79)
10	Y	K	Y	R	.	(SEQ ID NO:80)
25      11#						

\*Variant also contained Met226Ile.

#Variant E11 was a contaminant from library F (identical to the other 12 library F variants).

30

Upon randomization, Pro205 (Pro29) sorted to Thr or Tyr. Ser206 (Ser30) sorted to mixed residues, predominantly those having basic side chains, although Gly also appears twice (in sequences derived from the same variant). An inversion of side chains occurred for Arg207 (Arg31) and Tyr208 (Tyr32), the first of which sorted exclusively to Tyr and the second of which sorted primarily to Arg (seven variants) and Leu (four variants). This finding was particularly unexpected, given that Tyr208 stacks with Phe189 (Phe13) in the

structure and is conserved in the EGF sequence. See Jacobsen et al., *Biochemistry* 35:3402-17 (1996). At Leu209 (Leu33), the relatively conservative Met substitution was found in the majority of variants, but 5 Gly was also found.

*Library G - HRG- $\beta$ 1 211-216 (HRG- $\beta$ 1 EGF 35-40)*

HRG- $\beta$ 1 211-216 (HRG- $\beta$ 1 EGF 35-40) includes the first  $\beta$ -strand of the C-terminal subdomain of HRG- $\beta$ 1 10 EGF. The amino acid changes in the variants selected from this library are shown in Table 11.

Table 11  
*Library G Variants*

15

Variant No.	Position in HRG- $\beta$ 1					
	211	212	213	214	215	216
Wild-type	K	C	P	N	E	F
1, 5, 6, 10, 12	R	.	S	L	.	.
2	R	.	S	E	.	.
3	.	.	.	K	.	M
4	R	.	T	V	.	Y
7, 8	R	.	T	V	.	Y
9	.	.	N	S	.	.
11	R	.	K	K	.	.

Upon randomization, 10 out of 12 variants contained a Lys211Arg (Lys35Arg) mutation, thus retaining a 30 positive charge at this position, which lies between two cysteines. Pro213 (Pro37) sorted to mixed hydrophilic residues, and Asn214 (Asn38) sorted to a mixture of residues, with Leu and Val appearing most frequently. Glu215 (Glu39) was conserved in all 35 variants, and Phe216 (Phe40) was retained in eight out of 12 variants with a conservative Tyr substitution in three of the remaining variants.

*Library H - HRG- $\beta$ 1 217-220 (HRG- $\beta$ 1 41-44)*

The HRG- $\beta$ 1 217-220 (HRG- $\beta$ 1 EGF 41-44) library proved vulnerable to contamination by a high-affinity variant from library B (variant B5). This variant was 5 found in 11 out of 12 variants. In the single unaffected variant, the wild-type amino acid sequence was conserved except for an Asp219Glu (Asp43Glu) mutation. This result suggests that this region requires the wild-type or similar sequences for optimal 10 binding.

*Library I HRG- $\beta$ 1 222-226 (HRG- $\beta$ 1 EGF 46-50)*

HRG- $\beta$ 1 222-226 (HRG- $\beta$ 1 EGF 46-50) includes a short strand of  $\beta$ -sheet that aligns with the strand of  $\beta$ -sheet at HRG- $\beta$ 1 213-216 (HRG- $\beta$ 1 EGF 38-40). The 15 amino acid changes in the variants selected from this library are shown in Table 12.

Table 12  
20 Library I Variants

Variant No.	Position in HRG- $\beta$ 1				
	222	223	224	225	226
Wild-type	Q	N	Y	V	M (SEQ ID NO:89)
1, 4, 8	.	W	.	.	I (SEQ ID NO:90)
2, 3, 5-7, 9-12	.	H	.	.	I (SEQ ID NO:91)

Upon randomization of HRG- $\beta$ 1 222-226, only two types of 30 variants were found in the 12 sequenced, both having wild-type residues conserved at Gln222 (Gln46), Tyr224 (Tyr48), and Val225 (Val49), and both having a Met226Ile (Met50Ile) mutation. Asn223 (Asn47) sorted to His (nine variants) or Trp (three variants). The 35 strong affinity-enhancing effect of Met226Ile is evidenced by its presence in all variants sequenced from this library and a high frequency of occurrence in variants from several other libraries.

Library F - HRG- $\beta$ 1 178, 180, 198, and 200 (HRG- $\beta$ 1 EGF  
2, 4, 22 and 24)

When His178 (His2), Val180 (Val4), Met198 (Met22), and Lys200 (Lys24) were simultaneously randomized, only 5 one type of variant was found. His178, Val180, and Lys200 sorted to wild-type residues, and Met198 sorted to Lys. These variants additionally contained the spontaneous Met226Ile (Met50Ile) mutation, which gave the variants a significant selective advantage over 10 other sequences. It is striking that the wild-type His was found at position 178 because none of the 12 variants sequenced from library A contained His178.

15 *Conservation of HRG- $\beta$ 1 EGF Residues in Phage Display and Alanine Scanning Results*

Positions where alanine substitution strongly affected binding affinity tended to sort to the wild-type residue. See, for example, the data for positions at the junction between the N- and C-terminal 20 subdomains, (i.e., the  $\beta$ -turn at HRG- $\beta$ 1 191-195 [HRG- $\beta$ 1 EGF 15-19] and the loop at HRG- $\beta$ 1 217-220 [HRG- $\beta$ 1 EGF 41-44]) Additionally, positions where alanine 25 substitution produced less significant effects tended to undergo substantial mutation upon phage display, as seen for the helical stretch at HRG- $\beta$ 1 183-188 (HRG- $\beta$ 1 EGF 7-12).

30 *Analysis of the Impact of Selected Mutations on Receptor Affinity and Specificity*

Individual variants from each library were chosen 35 for phage production and further characterization of the mutated HRG- $\beta$ 1 EGPs ("variants") displayed on the phage. The choice of variants for further characterization was based on selection frequency, with a bias towards sequences not containing the advantageous Met226Ile (Met50Ile) substitution. In addition, phagemid vectors for use in producing phage

displaying mutated HRG- $\beta$ 1 EGFs containing various combinations of the above mutations ("combination variants") were prepared by Kunkel mutagenesis, using templates prepared from several of the above-described 5 variants. The amino acid substitutions in the combination variants are indicated in Figure 4. The affinities of the variants and combination variants for binding to ErbB-3-Ig (relative to the affinity of wild-type HRG- $\beta$ 1 EGF) were determined by phage ELISA, as 10 described in Example 1. The results are shown in Table 13. Some of the variants and combination variants were also tested for relative ErbB-4-Ig affinity to assess specificity.

**Table 13**  
**Affinities of Heregulin- $\beta$ 1 EGF Variants and**  
**Combination Variants for ErbB-3-Ig and ErbB-4-Ig**  
**as Determined by Phage ELISA**

	Construct	Phage ErbB-3	Phage ErbB-4
		EC <sub>50</sub> (wt) / EC <sub>50</sub> (mut)*	EC <sub>50</sub> (wt) / EC <sub>50</sub> (mut)
	HRG8	1	1
	HRG63	1.1 ± 0.8	
10	A1	0.55 ± 0.27	
	A2	0.87 ± 0.5	
	A3	0.96 ± 0.43	1.1 ± 0.4
	A4	<0.3	
	B3	4.7 ± 0.77	1.7 ± 0.5
15	B5	26 ± 20	
	B10	9.3	
	D1	11 ± 0.45	
	D4	2.9 ± 1.1	5.0 ± 3.7
	D10	2.1	
20	E2	28 ± 13	7.6
	E3	16	
	E6	6.6 ± 3.0	
	E8	17 ± 2.3	
	G1	1.2 ± 0.36	1.6
25	G4	0.86 ± 0.19	
	H5	1.5	
	I1	13 ± 11	
	I2	20 ± 20	10
	F1	4.4 ± 3.3	
30	HRG90	6.3 ± 3.1	
	HRG37	13 ± 15	
	HRG38	<0.3	
	HRG40	<0.3	
	HRG41	<0.3	
35	HRG48	49 ± 15	

Construct	Phage ErbB-3	Phage ErbB-4
	EC <sub>50</sub> (wt) / EC <sub>50</sub> (mut) <sup>*</sup>	EC <sub>50</sub> (wt) / EC <sub>50</sub> (mut)
HRG53	26 ± 16	
HRG54	12 ± 9.2	
HRG55	13 ± 11	
HRG56	31 ± 22	
5 HRG57	24 ± 16	
HRG58	58 ± 11	44
HRG59	26 ± 14	
HRG60	63 ± 11	
HRG61	29 ± 25	
10 HRG62	32 ± 14	
HRG71	79 ± 56	
HRG73	56 ± 6.6	16

\*Based on the wild-type HRG-β1 EGF-phage EC<sub>50</sub> (=135 ± 104 nM for ErbB-3-Ig, 163 ± 112 nM for ErbB-4-Ig) determined on during the same assay run. Shown are standard deviations for averages of 2-4 duplicate runs, or the average only for assays performed in duplicate for one run.

20

Variants from library A had EC<sub>50</sub> values very similar to wild-type HRG-β1 EGF. Variants from libraries B and D had significantly enhanced affinity for ErbB-3-Ig and ErbB-4-Ig, in the range of three to five times the wild-type affinity for selected variants not containing Met226Ile (Met50Ile). (See variants B3 and D4.) Substantially greater enhancements in affinity (up to 26-fold wild-type HRG-β1 EGF) were measured for variants that contained Met226Ile (Met50Ile). (See variants B5, B10, and D1).

30 Variants from library E showed even greater affinity enhancements. For example, variant E2, which differed from the library consensus sequence (Figure 3) at HRG-β1 206 and 208 (HRG-β1 EGF 30 and 32), had an affinity enhancement of 28-fold. The effects appear to 35 be associated with the amino acid substitutions at

HRG- $\beta$ 1 205-209 (HRG- $\beta$ 1 EGF 29-33) rather than the adjacent three-residue deletion, since the affinity for ErbB-3-Ig of a  $\Delta$ 202-204 ( $\Delta$ 26-28) control variant (HRG63) was similar to that of wild-type HRG- $\beta$ 1 EGF 5 (Table 13).

The single variant from library F, having Met198Lys (Met22Lys) and Met226Ile (Met50Ile) substitutions, showed an enhancement only slightly above that for Met226Ile alone, indicating a small 10 effect attributable to the Met198Lys mutation. Variants from library G showed little, if any, ErbB-3-Ig affinity enhancement. The single Asp219Glu (Asp43Glu) mutation from the lone library H variant provided a modest increase in affinity. The two 15 library I variants had significant enhancements in affinity for ErbB-3-Ig and ErbB-4-Ig. The enhancements were attributable to an approximately six-fold effect from the Met226Ile (Met50Ile) mutation (see variant HRG90), and an additional enhancement of about two- to 20 three-fold from Asn223 (Asn47) to Trp or His mutations.

Phage displaying combination variants containing variant A3 mutations performed poorly. The A3 + B3 combination had an EC<sub>50</sub> for ErbB-3-Ig similar to that of variant B3, but the other combinations tested did not 25 bind with detectable affinity. This could be due to a disadvantageous interaction of the Ser177Trp, His178Glu, or Lys181Pro (Ser1Trp, His2Glu, or Lys5Pro) mutations with mutations from the other libraries. The combination of the B3 and E2 mutations yielded slightly 30 diminished affinities relative to that of variant E2.

The combination of mutations from variants from the other libraries gave closer to additive behavior and resulted in the enhancement of EC<sub>50</sub> values by greater than 50-fold. The EC<sub>50</sub> values for the best 35 combination variants were close to the lower limit of the assay at the receptor coating concentration used (approximately 4 nM). Using lower levels of receptor

coat yielded sub-nanomolar EC<sub>50</sub> values for these combination variants, but did not allow measurement of wild-type affinity, due to minimal binding of wild-type HRG-β1 EGF phage. The best combination variants 5 contained the D4 sequence, either the B3 or E2 sequence, and either the single Met50Ile mutation or the I2 sequence.

In general, variants that exhibited enhancements 10 in affinity for ErbB-3-Ig also exhibited similar enhancements in affinity for ErbB-4-Ig.

*Expression, Purification, and Assay of Soluble HRG-β1 EGF Variants*

A number of variants were expressed in soluble 15 form (i.e., mutated HRG-β1 EGPs were expressed free of M13 pIII). To facilitate periplasmic expression of soluble variants, TAG codons were installed following HRG-β1 226 (HRG-β1 EGF 52) in the corresponding phagemids by Kunkel mutagenesis, and the resulting 20 constructs were transformed into 34B8 cells (genotype: tonAΔ phoAΔE15 Δ(argF-lac)169 deoC2 ompTΔ degP41 (ΔPstI-kanR)). The constructs included those for expressing variants A3, E2, and F1, and combination 25 variants HRG58 (D4+E2+M50I) and HRG73 (B3+D4+E2+I2), as well as the construct that expressed wild-type HRG-β1 EGF (HRG8).

Expression at levels of about 1 mg/L was achieved as follows. Cell cultures were grown to a density of OD<sub>550</sub> = 1.0 in LB medium containing 50 µg/mL 30 carbenicillin and used to inoculate modified AP5 medium at a 1/100 dilution. (Modified AP5 medium contained: 1.5 g/L glucose, 11 g/L Hycase SF, 0.6 g/L yeast extract, 0.19 g/L anhydrous MgSO<sub>4</sub> or 0.394 g/L MgSO<sub>4</sub>·7H<sub>2</sub>O, 1.07 g/L ammonium chloride, 35 3.73 g/L KCl, 1.2 g/L NaCl, 120 mL/L 1 M triethanol-amine [pH 7.4].)

Wild-type HRG- $\beta$ 1 EGF and variants thereof were purified to homogeneity from periplasmic shockates in a single reverse-phase HPLC step. Briefly, cells were harvested after 24 h of growth at 30°C ( $OD_{550} = 1.2$ ) by centrifugation at 4500 rpm, and the pellets were frozen in ethanol/dry ice for 2 h. Following resuspension and thawing in 5 mM MgCl<sub>2</sub>, 75 mM CaCl<sub>2</sub>, 1 mM phenyl methyl sulfonyl fluoride, and 10 mM Tris-HCl (pH 7.6), shocked cells were removed by centrifugation, leaving shockates. Shockates were filtered and chromatographed by semipreparative C18 reverse-phase HPLC using a gradient from 0-40% acetonitrile over 80 min, with a flow rate of 3 mL/min. Fractions shown by electrospray mass spectrometry to contain HRG- $\beta$ 1 EGF (or variants thereof) were lyophilized and resuspended in 1 mM EDTA, 10 mM Tris-HCl (pH 7.6). Proteins were found to be essentially homogeneous as determined by amino acid analysis and SDS-PAGE.

The affinities of the soluble variants for ErbB-Ig were determined by measuring inhibition of <sup>125</sup>I-HRG binding to ErbB-2/3, -3 and -4 receptor-Ig fusions, as previously described in Example 1. Although the ErbB-2/3-Ig preparation also contains ErbB-2/2 and 3/3 homodimers (as a result of coexpression of ErbB-2- and -3-Ig's), the displacement of <sup>125</sup>I-HRG should be predominantly from ErbB-2/3-Ig because of the approximately 100-fold higher affinity of wild-type HRG- $\beta$ 1 EGF for the 2/3-heterodimer versus the 3/3 homodimer.

The results are shown in Table 14.

Table 14  
*Binding and Activation Parameters for Soluble  
 Heregulin- $\beta$ 1 EGF Variants*

Construct	ErbB-3-Ig EC <sub>50</sub> (nM)	ErbB-4-Ig EC <sub>50</sub> (nM)	ErbB-2/3-Ig EC <sub>50</sub> (nM)	KIRA EC <sub>50</sub> (nM)
HRG8 (WT)	2.3 ± 0.2	1.5 ± 0.1	0.033 ± 0.003	0.212
A3	4.3 ± 0.2	2.1 ± 0.1	0.067 ± 0.007	0.182
E2	2.0 ± 0.2	2.4 ± 0.02	0.035 ± 0.007	0.092
F1	0.60 ± 0.04	0.26 ± 0.011	0.061 ± 0.002	0.151
HRG58	0.80 ± 0.01	0.30 ± 0.005	0.075 ± 0.006	0.129
HRG73	2.7 ± 0.1	0.31 ± 0.003	0.20 ± 0.006	0.173

The variants showed higher affinity for ErbB-3-Ig than did wild-type HRG- $\beta$ 1 EGF (up to 4-fold), although the affinity enhancements were less dramatic than determined by phage ELISA. Analysis in this format also revealed that the E2 mutations confer greatly enhanced affinity, and that the additional D4 and Met50Ile mutations (in construct HRG58) do not contribute additively. As observed in the phage ELISAs, the variants showed enhancements in affinity for ErbB-4-Ig that were similar to affinity-enhancements for ErbB-3-Ig. Variant affinities for ErbB-2/3-Ig were similar to the affinity of wild-type HRG- $\beta$ 1 EGF for the 2/3-heterodimer, although the maximally substituted construct (HRG72) bound 6-fold more weakly to ErbB-2/3-Ig than did wild-type HRG- $\beta$ 1 EGF.

The soluble variants were also assayed for their ability to stimulate tyrosine phosphorylation of the ErbB-2 receptor on MCF7 breast cancer carcinoma cells. This was accomplished in a KIRA-ELISA format as described in Sadick et al., *Analyt. Biochem.* 235:207-214, in which the ErbB-2 phosphorylation detected is

believed to be due primarily to the formation of ErbB-2/3 heterodimers.

Briefly,  $2 \times 10^5$  MCF-7 cells were added to each well of a flat-bottom 96-well culture plate and cultured overnight. The following morning the culture medium was replaced with medium containing a variant or HRG8 (wild-type) at concentrations ranging from 0 to 10 nM. The cells were stimulated at 37°C for 30 min, the culture medium was decanted. To lyse the cells and solubilize the receptors, 100  $\mu$ l of lysis buffer was added to each well. Lysis buffer consisted of 150 mM NaCl, 50 mM HEPES, 0.5% Triton-X100, 0.01% thimerosol, 30 kIU/ml aprotinin (ICN Biochemicals, Aurora, OH), 1 mM 4-(2-aminoethyl) benzenesulfonyl fluoride hydrochloride (AEBSF; ICN Biochemicals), and 2 mM sodium orthovanadate. The plate was then agitated gently on a plate shaker (Bellco Instruments, Vineland, NJ) for 60 min at room temperature.

While the cells were being solubilized, an ELISA microtiter plate (Nunc Maxisorp™, Inter Med, Denmark) that had been coated overnight at 4°C with the affinity-purified polyclonal anti-ErbB-2 ECD antibody (1.0  $\mu$ g/ml in 50 mM carbonate buffer (pH 9.6) was decanted, and blocked with block buffer (PBS, 0.5% BSA [Intergen Co., Purchase, NY], 0.01% thimerosol) for 60 min at room temperature with gentle agitation. After 60 min, the anti-ErbB-2 ECD-antibody coated plate was washed six times with wash buffer (PBS, 0.05% Tween 20™, 0.01% thimerosol) using an automated plate washer (ScanWasher 300, Skatron Instruments, Inc., Sterling, VA).

The lysate containing solubilized ErbB-2 from each cell-culture microtiter well was transferred to each anti-ErbB2 ECD antibody-coated and blocked ELISA well and incubated for 2 h at room temperature with gentle agitation. The unbound receptor was removed by washing with wash buffer, and 100  $\mu$ l of biotinylated 4G10

(antiphosphotyrosine antibody) diluted to 0.2  $\mu$ g/ml in dilution buffer (PBS, 0.5% BSA, 0.05% Tween 20<sup>TM</sup>, 5 mM EDTA, 0.01% thimerosol) was added to each well. After incubation for 2 h at room temperature, the plate 5 was washed, and 100  $\mu$ l horseradish peroxidase-conjugated streptavidin (Zymed Laboratories, S. San Francisco, CA), diluted 1:50000 in dilution buffer, was added to each well. The plate was incubated for 30 min at room temperature with gentle agitation. The free 10 avidin conjugate was washed away, and 100  $\mu$ l freshly prepared substrate solution (tetramethyl benzidine, TMB, two-component substrate kit, Kirkegaard and Perry, Gaithersburg, MD) was added to each well. The reaction was allowed to proceed for 10 min, after which the 15 color development was stopped by the addition of 1.0 M H<sub>3</sub>PO<sub>4</sub>.

The results are shown in Table 14. The EC<sub>50</sub> is the concentration of variant (or HRG8) required to achieve 20 50% maximal tyrosine phosphorylation. In general, the EC<sub>50</sub>'s for stimulation of phosphorylation by the variants tested did not differ substantially from the EC<sub>50</sub> for wild-type HRG- $\beta$ 1 EGF. In addition, the values correlated well with the IC<sub>50</sub>'s for binding to the receptor fusions above.

25

#### EXAMPLE 4

Selection of Heregulin- $\beta$ 1 EGF Domain Variants  
For ErbB-4 Receptor Binding  
Using Monovalent Phage Display

This example describes the selection of HRG- $\beta$ 1 30 variants for binding to the ErbB-4 receptor, and in particular, variants having a greater specificity for the ErbB-4 receptor, relative to the ErbB-3 receptor, than wild-type HRG- $\beta$ 1. Such variants have, for 35 example, a lower variant:wild-type EC<sub>50</sub> ratio for binding to ErbB-4-Ig than for binding to ErbB-3-Ig. The variants studied contained residues corresponding

to HRG- $\beta$ 1 177-244, which includes the minimal EGF-like domain (HRG- $\beta$ 1 177-228). In this example, "HRG- $\beta$ 1 EGF" refers to the region of the EGF-like domain extending from residues 177-244. Residue numbers are expressed 5 in terms of position in 645-amino acid native human HRG- $\beta$ 1 and, in parentheses, in terms of position in HRG- $\beta$ 1 EGF (i.e., HRG- $\beta$ 1 EGF 1-68).

The variants were produced by randomization at His178, Leu179, and Arg207 (His2, Leu3, and Arg31). 10 These residues were chosen because alanine scanning (Example 2) indicated that the substitution of alanine at these positions resulted in a significantly greater loss of affinity for the ErbB-3 receptor, as compared to the ErbB-4 receptor, suggesting that these residues 15 may be more important for ErbB-3 receptor binding than for ErbB-4 receptor binding. Additionally, these residues are predicted to be proximal to one another on the surface of the HRG- $\beta$ 1 molecule, potentially forming a binding site.

20

#### *Phage Library Screening for ErbB-4-Ig Binding*

Variants of HRG- $\beta$ 1 EGF were prepared and selected for binding to ErbB-4-Ig using monovalent phage display, according to the method of Bass et al., 25 *Proteins* 8:309-14 (1990). Briefly, the HRG- $\beta$ 1 EGF phagemid vector was pHRG2-p3 (described in Example 1), in which HRG- $\beta$ 1 177-244 was fused to a C-terminal fragment of the M13 coat protein pIII. Kunkel mutagenesis was performed to introduce stop codons into 30 this vector at His178, Leu179, and Arg207 (His2, Leu3, and Arg31) to ensure that the starting vector could not express the wild-type polypeptide.

These sites were then randomized by Kunkel mutagenesis to produce an HRG- $\beta$ 1 EGF library. Phage 35 displaying mutated HRG- $\beta$ 1 EGFs monovalently were produced from the library. See Bass et al., *supra*. These phage were then sorted against ErbB-4-Ig

homodimers immobilized on an ELISA plate. Bound phage were eluted and used to reinfect host cells, which were used to produce new phage. Half of the phage from the first round of sorting was sorted against immobilized ErbB-4-Ig for three additional rounds of sorting. The other half of the phage from the first round was sorted against immobilized ErbB-4-Ig for three additional rounds in the presence of soluble ErbB-3-Ig (10 nM). Sorting in the presence of soluble ErbB-3-Ig (i.e., "counter-selecting" against ErbB-3-Ig) was expected to remove variants with higher affinity for ErbB-3-Ig, allowing enrichment of those with higher affinity for ErbB-4-Ig in each round of sorting. After sorting, twelve clones from each of the two resultant libraries were sequenced.

#### *Construction of Initial Phage Library*

The initial phage library was constructed by Kunkel mutagenesis using uracil-containing single-stranded DNA template. TAA and TGA stop codons were installed at positions selected for randomization to generate a custom template that eliminated wild-type background from the pools. Positions were fully randomized by mutation to NNS codons (where N is any of the four bases and S is either G or C). Two mutagenesis oligonucleotides were used, one to randomize His178 and Leu179 (His2 and Leu3) and one to randomize Arg207 (Arg31). The oligonucleotides contained 15-base overhangs on either side of the randomized residues.

The final mutagenesis reaction mixture was electro-transformed into XL-1 blue cells (Stratagene, Inc., La Jolla, CA), according to the manufacturer's protocol. The transformed cells were then infected with  $10^{11}$  pfu M13K07 helper phage (Promega Corp., Madison, WI), and phage stocks (about  $10^{14}$  phagemid/mL) were prepared as described in Example 1.

At least  $10^8$  transformants were obtained, indicating that the library had excellent representation of the possible amino acid sequence combinations.

5

*Selection of Phage for ErbB-4-Ig Binding*

Monovalent phage were prepared and the selection performed on ErbB-4-Ig prebound to microtiter plates via capture with polyclonal antibodies to the human Fc fragment, as described in Example 1. Approximately  $10^{12}$  phage in 100  $\mu$ L binding buffer (PBS, 0.1% BSA, 0.05% Tween 20<sup>TM</sup>) were applied to an ErbB-4-Ig-coated well and a control well to which no ErbB-4-Ig had been added. After the first round of sorting, half of the resultant phage (hereafter the "counter-selected library") were sorted in the presence of 10 mM ErbB-3-Ig in the binding buffer. Following a 2 h incubation at room temperature, the plates were washed extensively (12x) and phage eluted by adding 100  $\mu$ L of a solution of 50 mM HCl and 0.05% Tween<sup>TM</sup> 20 and shaking for 10 min.

Eluates were neutralized with 10  $\mu$ L 1 M Tris-HCl (pH 8.0) and 20  $\mu$ L used for titration on log-phase XL-1 blue cells. The remainder was used to infect 1 mL of log-phase XL-1 blue cells (30 min at 37°C), which were then superinfected with  $2 \times 10^{10}$  pfu M13KO7 phage and grown in 25 mL 2YT broth (16 g/L tryptone, 10 g/L yeast extract, 5 g/L NaCl) containing 50  $\mu$ g/mL carbenicillin for 18-24 h. Phage were harvested as described above and the cycle repeated.

After round four of selection, twelve clones from each library were randomly picked and sequenced by the dideoxy method. See Sanger et al., PNAS USA 74:5463-67 (1977). The amino acids at the randomized positions deduced from the DNA sequences are shown in Table 15 (a " ." indicates a residue that is identical to the wild-type residue).

Table 15  
*Mutations and Affinities for ErbB-3- and ErbB-4-Igs  
 in Phage ELISA*

5     Four Rounds of Sorting for ErbB-4-Ig Binding  
 (No Counter-Selection) :

	<u>Wild-type</u>	H	L	R	#Siblings <sup>a</sup>	ErbB-4 <u>EC<sub>50</sub></u>	ErbB-3 <u>EC<sub>50</sub></u>	Mut/WT <sup>b</sup>	ErbB-3 <u>EC<sub>50</sub></u>	Mut/WT
10	Clones	.	M	.	7	1.5			1.2	
		W	.	.	2	1.7			1.2	
		E	.	.	2	1.7			9.5	
		.	V	.	1	1.6			1.5	

15

Four Rounds of Sorting for ErbB-4-Ig Binding  
 With ErbB-3-Ig Counter-Selection:

20	Clones	.	.	P	7	1.3		6.1		
		L	.	.	1	1.7		6.4		
		L	.	.	1	1.2		1.4		
		D	V	.	1	2.0		2.2		
		E	V	.	1	1.7		0.8		
25		T	M	.	1	1.6		1.4		

\*HRG- $\beta$ 1 228-331 (HRG- $\beta$ 1 EGF 52-55) were spontaneously deleted and replaced by a single Met residue.

30     <sup>a</sup>Number of variants having this sequence (out of the twelve sequenced for each library).

35     <sup>b</sup>EC<sub>50</sub> for the variant divided by the EC<sub>50</sub> for wild-type HRG- $\beta$ 1 177-244 expressed monovalently on phage

One variant predominated in each library, being represented in seven of the twelve clones sequenced from each library. The predominant variant from the 40 library counter-selected against ErbB-3-Ig sorted back to the wild-type residue at positions His178 and Leu179 (His2 and Leu3) and had Pro at Arg207 (Arg31). The predominant variant from the library that was sorted without counter-selection sorted to wild-type at 45 positions His178 and Arg207 (His2 and Arg31) and had Met at Leu179 (Leu3). In variants from each of the libraries, there was a spontaneous substitution of Met for HRG- $\beta$ 1 228-231 (HRG- $\beta$ 1 EGF 52-55).

*Analysis of the Impact of Mutations on Receptor Affinity and Specificity*

Receptor binding affinities were measured by phage ELISA for all unique variants from each library, as 5 described in Example 1. The results are shown in Table 15. The affinities of the variants for ErbB-3-Ig and ErbB-4-Ig were determined to assess specificity.

The affinities of most variants for the ErbB receptor-Ig fusions were reduced between about 1.2-fold 10 and 2.2-fold. Only one variant showed a slight enhancement in affinity, and only for ErbB-3-Ig. However, three variants had affinities for ErbB-4-Ig that were less than two-fold below the affinity of wild-type HRG- $\beta$ 1, whereas their affinities for 15 ErbB-3-Ig were 6- to 9-fold below the affinity of wild-type HRG- $\beta$ 1. All of these variants sorted back to the wild-type residue at Leu179 (Leu3). One variant sorted to Glu at His178 (His2) and to wild-type at Arg207 (Arg31). Another variant sorted to wild-type at His178 20 (His2) and to Pro at Arg 207 (Arg31). This was the predominant variant in the counter-selected library.

The third variant sorted to Leu at His178 (His2) and to wild-type at Arg207 (Arg31) and also had the spontaneous substitution of Met for HRG- $\beta$ 1 228-231 25 (HRG- $\beta$ 1 EGF 52-55). The affinity of this variant for ErbB-3-Ig was reduced 6.4 fold, whereas another variant with the same sequence at His178, Leu179, and Arg207 (His2, Leu3, and Arg31), but lacking the spontaneous substitution, retained approximately wild-type affinity 30 for ErbB-3-Ig. Thus, the reduction in affinity for ErbB-3-Ig binding is largely attributable to this spontaneous substitution. Because HRG- $\beta$ 1 228-231 35 (HRG- $\beta$ 1 EGF 52-55) is unlikely to be proximal to the randomized region on the surface of the HRG- $\beta$ 1 molecule, the data suggest that at least two distinct regions of HRG- $\beta$ 1 are important for ErbB receptor

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binding, namely residues His178, Leu179, and Arg207  
(His2, Leu3, and A<sup>-</sup>31) and HRG- $\beta$ 1 228-231 (HRG- $\beta$ 1 EGF  
52-55).

Two of the three variants exhibiting enhanced  
5 specificity for ErbB-4-Ig binding accounted for eight  
of the twelve clones isolated from the counter-selected  
library. The other variant accounted for only two of  
the twelve clones isolated from the library that was  
sorted without counter-selection. Thus, counter-  
10 selection against ErbB-3-Ig produced a significant  
enrichment in variants exhibiting greater specificity  
for ErbB-4-Ig, relative to ErbB-3-Ig, than that of  
wild-type HRG- $\beta$ 1.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5

(i) APPLICANT: Ballinger, Marcus D.  
Jones, Jennifer T.  
Fairbrother, Wayne J.  
Sliwkowski, Mark X.  
10 Wells, James A.  
Genentech, Inc.

(ii) TITLE OF INVENTION: HEREGULIN VARIANTS

15

(iii) NUMBER OF SEQUENCES: 92

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESS: Skjerven, Morrill, MacPherson, et al.  
(B) STREET: 25 Metro Drive, Suite 700  
20 (C) CITY: San Jose  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 95110

25

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Pending  
(B) FILING DATE: 10-FEB-1998

35

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/799,054  
(B) FILING DATE: 10-FEB-1997  
(C) CLASSIFICATION:

40

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Haliday, Emily M.  
(B) REGISTRATION NUMBER: 38,903  
(C) REFERENCE/DOCKET NUMBER: M-4761-1P PCT

45

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (408) 453-9200  
(B) TELEFAX: (408) 453-7979

50 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
 1 5 10 15

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
 20 25 30

20 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
 35 40 45

Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Ala  
 50 55 60

25

Glu Glu Leu Tyr Gln Lys Arg  
 65 70

30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

40

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
 1 5 10 15

50 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
 20 25 30

Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn  
 35 40 45

Val Pro Met Lys Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln  
 50 55 60

5 Lys Arg  
 65

## (2) INFORMATION FOR SEQ ID NO:3:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant  
 15 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
 1 5 10 15  
 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
 30 20 25 30  
 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
 35 40 45  
 35 Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr Gln Lys Arg  
 50 55 60

## (2) INFORMATION FOR SEQ ID NO:4:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant  
 45 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 50 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
 1 5 10 15

5 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
 20 25 30

Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
 35 40 45

10 Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro  
 50 55 60

Glu  
 15 65

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

25 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: Rattus rattus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

35 Ser His Leu Ile Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
 1 5 10 15

Gly Gly Glu Cys Phe Thr Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
 20 25 30

40 Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn  
 35 40 45

45 Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr Gln  
 50 55 60

Lys Arg  
 65

50 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid

2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus rattus

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

15 Ser His Leu Ile Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15

Gly Gly Glu Cys Phe Thr Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
20 25 30

20 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
35 40 45

Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Ala  
50 55 60

25

Glu Glu Leu Tyr Gln Lys Arg  
65 70

30

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

35

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus rattus

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser His Leu Ile Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15

50 Gly Gly Glu Cys Phe Thr Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
20 25 30

Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
35 40 45

Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr Gln Lys Arg  
 50                        55                        60

## 5 (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 64 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

15 (ii) MOLECULE TYPE: protein

15 (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Rattus rattus

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser His Leu Ile Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
 1                        5                        10                        15

25 Gly Gly Glu Cys Phe Thr Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
 20                        25                        30

Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn  
 30                        35                        40                        45

Val Pro Met Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu  
 50                        55                        60

35

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 81 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

45 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Rattus rattus

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser His Leu Ile Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

1	5	10	15													
Gly	Gly	Glu	Cys	Phe	Thr	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
				20			25							30		
5	Leu	Cys	Lys	Cys	Gln	Pro	Gly	Phe	Thr	Gly	Ala	Arg	Cys	Thr	Glu	Asn
				35				40						45		
10	Val	Pro	Met	Phe	Tyr	Ser	Met	Thr	Ser	Arg	Arg	Lys	Arg	Gln	Glu	Thr
				50			55							60		
	Glu	Lys	Pro	Leu	Glu	Arg	Lys	Leu	Phe	His	Ser	Leu	Val	Lys	Glu	Ser
				65			70							75		80
15	Lys															

## (2) INFORMATION FOR SEQ ID NO:10:

20           (i) SEQUENCE CHARACTERISTICS:  
               (A) LENGTH: 65 amino acids  
               (B) TYPE: amino acid  
               (C) STRANDEDNESS: not relevant  
               (D) TOPOLOGY: not relevant

25           (ii) MOLECULE TYPE: protein

30           (iii) HYPOTHETICAL: NO

35           (vi) ORIGINAL SOURCE:  
               (A) ORGANISM: Homo sapiens

35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:															
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
1				5				10						15		
40	Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr
					20			25						30		
	Leu	Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr
					35			40						45		
45	Val	Met	Ala	Ser	Phe	Tyr	Ser	Thr	Ser	Thr	Pro	Phe	Leu	Ser	Leu	Pro
					50			55						60		

50           Glu  
               65

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 65 amino acids

20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

15 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
20 25 30

20 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
35 40 45

25 Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro  
50 55 60

Glu  
65

30 (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 65 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

40 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15

50 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
20 25 30

Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr

35

40

45

Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro  
 50 55 60

5

Glu  
 65

## (2) INFORMATION FOR SEQ ID NO:13:

10

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

15

(ii) MOLECULE TYPE: protein

20

- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Gallus domesticus

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ser His Leu Thr Lys Cys Asp Ile Lys Gln Lys Ala Phe Cys Val Asn  
 1 5 10 15

30

Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro Asn Pro Pro Arg Tyr  
 20 25 30

Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
 35 40 45

35

Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Ala  
 50 55 60

40

Glu Glu Leu Tyr Gln Lys Arg  
 65 70

## (2) INFORMATION FOR SEQ ID NO:14:

45

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

50

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

5           Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
        1                       5                       10                       15

10          Gly Gly Glu Cys Phe Met Val Lys Asp Pro Ser Arg Tyr Leu Cys Lys  
        20                       25                       30

15          Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala  
        35                       40                       45

15       Ser

## (2) INFORMATION FOR SEQ ID NO:15:

20       (i) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 48 amino acids  
           (B) TYPE: amino acid  
           (C) STRANDEDNESS: not relevant  
           (D) TOPOLOGY: not relevant

25       (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30       (vi) ORIGINAL SOURCE:  
           (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

35       Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His  
        1               5                       10                       15

40       Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn  
        20               25                       30

45       Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Arg  
        35               40                       45

## (2) INFORMATION FOR SEQ ID NO:16:

50       (i) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 49 amino acids  
           (B) TYPE: amino acid  
           (C) STRANDEDNESS: not relevant  
           (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: Not relevant (recombinant)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

10 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15Gly Gly Glu Cys Phe Met Val Lys Asp Pro Ser Arg Tyr Leu Cys Lys  
20 25 3015 Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Ile Ala  
35 40 4520 Ser  
20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

30 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: Not relevant (recombinant)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

40 Trp Glu Leu Val Pro Cys Gly Trp Asp Arg Glu Gly Phe Cys Val Asn  
1 5 10 15Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
20 25 3045 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
35 40 4550 Val Ile Ala Ser  
50

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

5

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Trp	Glu	Leu	Val	Pro	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn
1															15

Gly	Gly	Glu	Cys	Tyr	Lys	Val	Arg	Ile	Tyr	Gly	Tyr	Leu	Met	Cys	Lys
20															30

Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Ile	Ala
35														45	

25 Ser

(2) INFORMATION FOR SEQ ID NO:19:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

35

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Trp	Glu	Leu	Val	Pro	Cys	Gly	Trp	Asp	Arg	Glu	Gly	Phe	Cys	Val	Asn
1															15

Gly	Gly	Glu	Cys	Tyr	Lys	Val	Arg	Ile	Tyr	Gly	Tyr	Leu	Met	Cys	Lys
50															30

Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Ile	Ala
35														45	

Ser

## (2) INFORMATION FOR SEQ ID NO:20:

5

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

10

(ii) MOLECULE TYPE: peptide

15

(iii) HYPOTHETICAL: NO

15

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Not relevant (recombinant)

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Trp	Glu	Leu	Val	Pro	Cys	Gly	Trp	Asp	Arg	Glu	Gly	Phe	Cys	Val	Asn
1															15

25

Gly	Gly	Glu	Cys	Tyr	Lys	Val	Arg	Ile	Tyr	Arg	Tyr	Arg	Met	Cys	Lys
20								25							30

30

Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Ile	Ala
35								40							45

Ser

## (2) INFORMATION FOR SEQ ID NO:21:

35

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

40

(ii) MOLECULE TYPE: peptide

45

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Not relevant (recombinant)

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn
1.															15

Gly Gly Glu Cys Phe Met Val Lys Asp Tyr Gly Tyr Leu Met Cys Lys  
 20 25 30

Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Ile Ala  
 5 35 40 45

Ser

10 (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

15 (ii) MOLECULE TYPE: peptide

20 (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Not relevant (recombinant)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser His Leu Val Lys Cys Gly Glu Glu Arg Glu Gly Phe Cys Val Asn  
 1 5 10 15

30 Gly Gly Glu Cys Tyr Arg Val Lys Thr Leu Ser Asn Pro Ser Arg Tyr  
 20 25 30

Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
 35 40 45

Val Met Ala Ser  
 50

40 (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

45 (ii) MOLECULE TYPE: peptide

50 (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Not relevant (recombinant)



(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: Not relevant (recombinant)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

10 Ser His Leu Val Lys Cys Gly Glu Glu Arg Glu Gly Phe Cys Val Asn  
1 5 10 15

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
20 25 30

15 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
35 40 45

20 Val Ile Ala Ser  
50

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

30 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: Not relevant (recombinant)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

40 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15

Gly Gly Glu Cys Tyr Arg Val Lys Thr Tyr Gly Tyr Leu Met Cys Lys  
20 25 30

45 Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala  
35 40 45

Ser

50

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

5 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

10 (vi) ORIGINAL SOURCE:  
      (A) ORGANISM: Not relevant (recombinant)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15

20 Gly Gly Glu Cys Tyr Arg Val Lys Thr Tyr Gly Tyr Tyr Leu Met Cys Lys  
20 25 30

Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Ile Ala  
           35                 . . 40                                   45

25  
Ser

(2) INFORMATION FOR SEQ ID NO:28:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

50 Gly Gly Glu Cys Tyr Arg Val Lys Thr Leu Ser Asn Pro Ser Arg Tyr  
20 25 30

Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr

35

40

45

Val Ile Ala Ser  
50

5

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

15

- (ii) MOLECULE TYPE: peptide

20

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Not relevant (recombinant)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

25 Ser His Leu Val Lys Cys Gly Glu Glu Arg Glu Gly Phe Cys Val Asn  
1                       5                       10                       15

Gly Gly Glu Cys Tyr Arg Val Lys Thr Leu Ser Asn Pro Ser Arg Tyr  
20                      25                       30

30 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
35                      40                       45

35 Val Ile Ala Ser  
50

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

45

- (ii) MOLECULE TYPE: peptide

50

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Not relevant (recombinant)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser His Leu Val Lys Cys Gly Glu Glu Arg Glu Gly Phe Cys Val Asn  
 1 5 10 15

5 Gly Gly Glu Cys Phe Met Val Lys Asp Tyr Gly Tyr Leu Met Cys Lys  
 20 25 30

Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Ile Ala  
 35 40 45

10

Ser

## (2) INFORMATION FOR SEQ ID NO:31:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

20

- (ii) MOLECULE TYPE: peptide

25

- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Not relevant (recombinant)

30

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ser His Leu Val Lys Cys Gly Glu Glu Arg Glu Gly Phe Cys Val Asn  
 1 5 10 15

35

Gly Gly Glu Cys Tyr Arg Val Lys Thr Tyr Gly Tyr Leu Met Cys Lys  
 20 25 30

40

Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Ile Ala  
 35 40 45

Ser

45

## (2) INFORMATION FOR SEQ ID NO:32.

50

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

10 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15

Gly Gly Glu Cys Tyr Arg Val Lys Thr Tyr Gly Tyr Leu Met Cys Lys  
20 25 30

15 Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln His Tyr Val Ile Ala  
35 40 45

Ser  
20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

30 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: Not relevant (recombinant)

40

Ser His Leu Val Lys Cys Gly Glu Glu Arg Glu Gly Phe Cys Val Asn  
1 5 10 15

Gly Gly Glu Cys Tyr Arg Val Lys Thr Tyr Gly Tyr Leu Met Cys Lys  
20 25 30

Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln His Tyr Val Ile Ala  
35 40 45

50 Ser

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
5 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Gly Gly Ser  
1

20 (2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
25 (B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

30 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Gly Gly Ser Gly Gly Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:36:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
45 (D) TOPOLOGY: not relevant

50 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Thr Arg Asp Lys Thr  
1 5

10

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

15

(ii) MOLECULE TYPE: peptide

20

(iii) HYPOTHETICAL: NO

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asp Asp Asp Asp Lys

1 5

(2) INFORMATION FOR SEQ ID NO:38:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

40

(ii) MOLECULE TYPE: peptide

45

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser His Leu Val Lys  
1 5

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Not relevant (recombinant)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Trp Arg Leu Val Pro  
1 5

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Not relevant (recombinant)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Trp Ser Leu Gln Pro  
1 5

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

10 Trp Glu Leu Val Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:42:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

20

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: 'NO'

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Trp Ser Leu Val Lys  
1 5

35 (2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

40 (ii) MOLECULE TYPE: peptide

45 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Trp Ser Leu Ile Pro

1 5

## (2) INFORMATION FOR SEQ ID NO:44:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

10 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

15 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Trp Arg Leu Val Ala  
1 5

## 25 (2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
30 (C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

35 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Trp -Ala Leu Val Pro  
45 1 5

## (2) INFORMATION FOR SEQ ID NO:46:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide  
(iii) HYPOTHETICAL: NO  
5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Trp Ser Leu Gln Lys  
1 5

15 (2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
20 (C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant  
  
(ii) MOLECULE TYPE: peptide  
  
25 (iii) HYPOTHETICAL: NO  
  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Trp Glu Leu Val Ala  
35 1 5

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
40 (D) TOPOLOGY: not relevant  
  
45 (ii) MOLECULE TYPE: peptide  
  
(iii) HYPOTHETICAL: NO  
  
(vi) ORIGINAL SOURCE:  
50 (A) ORGANISM: Not relevant (recombinant)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Trp Ser Leu Glu Pro  
1 5

5 (2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
10 (C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

15 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ala Glu Lys Glu Lys Thr  
25 1 5

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

35 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
40 (A) ORGANISM: Not relevant (recombinant)

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:  
Gly Val Gly Arg Asp Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:51:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

5 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

15 Gly Gly Glu Arg Glu Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:52:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: 'not relevant'

25 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: Not relevant (recombinant)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly Glu Glu Arg Glu Gly  
1 5

40 (2) INFORMATION FOR SEQ ID NO:53:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

45 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

Sequence Description: SEQ ID NO:53:

5           Gly Trp Asp Arg Glu Gly  
      1               5

## (2) INFORMATION FOR SEQ ID NO:54:

10           (i) SEQUENCE CHARACTERISTICS:  
            (A) LENGTH: 6 amino acids  
            (B) TYPE: amino acid  
            (C) STRANDEDNESS: not relevant  
            (D) TOPOLOGY: not relevant

15           (ii) MOLECULE TYPE: peptide

            (iii) HYPOTHETICAL: NO

20           (iv) ORIGINAL SOURCE:  
            (A) ORGANISM: Not relevant (recombinant)

25           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

      Gly Val Gln Arg Glu Gly  
      1               5

## (2) INFORMATION FOR SEQ ID NO:55:

30           (i) SEQUENCE CHARACTERISTICS:  
            (A) LENGTH: 6 amino acids  
            (B) TYPE: amino acid  
            (C) STRANDEDNESS: not relevant  
            (D) TOPOLOGY: not relevant

35           (ii) MOLECULE TYPE: peptide

            (iii) HYPOTHETICAL: NO

40           (iv) ORIGINAL SOURCE:  
            (A) ORGANISM: Not relevant (recombinant)

45           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

      Gly Glu Glu Arg Ala Gly  
      1               5

## (2) INFORMATION FOR SEQ ID NO:56:

50           (i) SEQUENCE CHARACTERISTICS:  
            (A) LENGTH: 6 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

5       (ii) MOLECULE TYPE: peptide

         (iii) HYPOTHETICAL: NO

         (vi) ORIGINAL SOURCE:

10       (A) ORGANISM: Not relevant (recombinant)

15       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

         Gly Lys Glu Arg Glu Gly  
          1              5

20       (2) INFORMATION FOR SEQ ID NO:57:

         (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

25       (ii) MOLECULE TYPE: peptide

         (iii) HYPOTHETICAL: NO

30       (vi) ORIGINAL SOURCE:

         (A) ORGANISM: Not relevant (recombinant)

35       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

         Thr Asn Ser Arg Glu Gly  
          1              5

40       (2) INFORMATION FOR SEQ ID NO:58:

         (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

45       (ii) MOLECULE TYPE: peptide

         (iii) HYPOTHETICAL: NO

         (vi) ORIGINAL SOURCE:

         (A) ORGANISM: Not relevant (recombinant)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

5 Asp Lys Ser Arg Glu Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:59:

(ii) MOLECULE TYPE: peptide

20           (iii) HYPOTHETICAL: NO

             (vi) ORIGINAL SOURCE:  
             (A) ORGANISM: Not relevant (recombinant)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Gly Glu Asp Arg Lys Gln  
1 5

30 (2) INFORMATION FOR SEQ ID NO:60:

35                   (i) SEQUENCE CHARACTERISTICS:  
                      (A) LENGTH: 6 amino acids  
                      (B) TYPE: amino acid  
                      (C) STRANDEDNESS: not relevant  
                      (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

50 Gly Arg Glu Arg Glu Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

10                   (iii) HYPOTHETICAL: NO  
                     (vi) ORIGINAL SOURCE:  
                      (A) ORGANISM: *Homo sapiens*

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Val Asn Gly Gly Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:62:

25                   (i) SEQUENCE CHARACTERISTICS:  
                      (A) LENGTH: 5 amino acids  
                      (B) TYPE: amino acid  
                      (C) STRANDEDNESS: not relevant  
                      (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

30 *ANALYTICAL HYPOTHETICALS* NO.

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

40 Val Asn Gly Gly Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:63:

45           (i) SEQUENCE CHARACTERISTICS:  
               (A) LENGTH: 5 amino acids  
               (B) TYPE: amino acid  
               (C) STRANDEDNESS: not relevant  
               (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Val Asn Gly Gly Val  
1 5

10

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
15 (B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

20

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

25

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Val Asn Gly Gly Gln  
1 5

35

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
40 (C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

45

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

50

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Phe Met Val Lys Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

10 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Not relevant (recombinant)

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

20 Tyr Lys Val Arg Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

30 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Phe Arg Val Lys Thr  
1 5

45 (2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

50 (ii) MOLECULE TYPE: peptide

5

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

10

Tyr Arg Val Lys Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:68:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

20

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: ,NO

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant),

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Tyr Met Ile Lys Tyr  
1 5

35

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

40

(ii) MOLECULE TYPE: peptide

45

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Tyr Met Val Lys Thr

1                   5

(2) INFORMATION FOR SEQ ID NO:71:

5                 (i) SEQUENCE CHARACTERISTICS:  
                  (A) LENGTH: 5 amino acids  
                  (B) TYPE: amino acid  
                  (C) STRANDEDNESS: not relevant  
                  (D) TOPOLOGY: not relevant

10               (ii) MOLECULE TYPE: peptide

                 (iii) HYPOTHETICAL: NO

15               (vi) ORIGINAL SOURCE:  
                  (A) ORGANISM: Not relevant (recombinant)

20               (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Arg Val Arg Thr  
1                   5'

25               (2) INFORMATION FOR SEQ ID NO:72:

30               (i) SEQUENCE CHARACTERISTICS:  
                  (A) LENGTH: 5 amino acids  
                  (B) TYPE: amino acid  
                  (C) STRANDEDNESS: not relevant  
                  (D) TOPOLOGY: not relevant

                 (ii) MOLECULE TYPE: peptide

35               (iii) HYPOTHETICAL: NO

                 (vi) ORIGINAL SOURCE:  
                  (A) ORGANISM: Homo sapiens

40

                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

45               Pro Ser Arg Tyr Leu  
                  1                   5

(2) INFORMATION FOR SEQ ID NO:73:

50               (i) SEQUENCE CHARACTERISTICS:  
                  (A) LENGTH: 5 amino acids  
                  (B) TYPE: amino acid  
                  (C) STRANDEDNESS: not relevant  
                  (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

    Thr Pro Tyr Leu Met  
    1               5

15 (2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
20 (C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE; peptide

25 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

    Tyr Gly Tyr Leu Met  
    1               5

35 (2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:  
40 (A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

45 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
50 (A) ORGANISM: Not relevant (recombinant)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Tyr Arg Tyr Arg Met  
1 5

5 (2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- 10 (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

15 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Not relevant (recombinant)

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Thr His Tyr Arg Gly  
25 1 5

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- 30 (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

35 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Not relevant (recombinant)

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Thr His Tyr Arg Met  
1 5

(2) INFORMATION FOR SEQ ID NO:78:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

5 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

15            Tyr Lys Tyr Arg Met  
              1                      5

(2) INFORMATION FOR SEQ ID NO:79:

20                   (i) SEQUENCE CHARACTERISTICS:  
                      (A) LENGTH: 5 amino acids  
                      (B) TYPE: amino acid  
                      (C) STRANDEDNESS: not relevant  
                      (D) TOPOLOGY: not relevant

25 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
30 (A) ORGANISM: Not relevant (recombinant)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

35 Thr Lys Tyr Arg Gly

(2) INFORMATION FOR SEQ ID NO:80:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
45 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Not relevant (recombinant)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

5           Tyr Lys Tyr Arg Leu  
      1               5

## (2) INFORMATION FOR SEQ ID NO:81:

10           (i) SEQUENCE CHARACTERISTICS:  
            (A) LENGTH: 6 amino acids  
            (B) TYPE: amino acid  
            (C) STRANDEDNESS: not relevant  
            (D) TOPOLOGY: not relevant

15           (ii) MOLECULE TYPE: peptide

            (iii) HYPOTHETICAL: NO

20           (vi) ORIGINAL SOURCE:  
            (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

25           Lys Cys Pro Asn Glu Phe  
      1               5

## (2) INFORMATION FOR SEQ ID NO:82:

30           (i) SEQUENCE CHARACTERISTICS:  
            (A) LENGTH: 6 amino acids  
            (B) TYPE: amino acid  
            (C) STRANDEDNESS: not relevant  
            (D) TOPOLOGY: not relevant

35           (ii) MOLECULE TYPE: peptide

            (iii) HYPOTHETICAL: NO

40           (vi) ORIGINAL SOURCE:  
            (A) ORGANISM: Not relevant (recombinant)

## 45           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

50           Arg Cys Ser Leu Glu Phe  
      1               5

## (2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 6 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

5 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: Not relevant (recombinant)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Arg Cys Ser Glu Glu Phe  
1 5

20 (2) INFORMATION FOR SEQ ID NO:84:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Lys Cys Pro Lys Glu Met  
1 5

40 (2) INFORMATION FOR SEQ ID NO:85:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

50 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

5  
Arg Cys Thr Val Glu Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:86:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
15 (D) TOPOLOGY: not relevant  
  
(ii) MOLECULE TYPE: peptide  
  
(iii) HYPOTHETICAL: NO  
  
20 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Arg Cys Thr Val Glu Tyr  
1 5

30 (2) INFORMATION FOR SEQ ID NO:87:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant  
  
(ii) MOLECULE TYPE: peptide  
  
  
(A) ORGANISM: Not relevant (recombinant)

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

50 Lys Cys Asn Ser Glu Phe  
1 5

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
5 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Arg Cys Lys Lys Glu Phe  
1 5

20 (2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
25 (B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

30 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

35 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

40 Gln Asn Tyr Val Met  
1 5

(2) INFORMATION FOR SEQ ID NO:90:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

50 (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Gln Trp Tyr Val Ile  
1 5

10

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
15 (B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

20

(ii) MOLECULE TYPE: peptide

25

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Not relevant (recombinant)

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

35

Gln His Tyr Val Ile  
1 5

40

(2) INFORMATION FOR SEQ ID NO:92:

45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

50

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

55

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15

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Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr  
20 25 30

Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr  
5 35 40 45

Val Met Ala Ser  
50